

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Darnell Jr., James E.  
Schindler, Christian W.  
Fu, Xian-Yuan  
Wen, Zilong  
Zhong, Zhong
- (ii) TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN  
SEQUENCES AND METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Klauber & Jackson
  - (B) STREET: 411 Hackensack Avenue
  - (C) CITY: Hackensack
  - (D) STATE: New Jersey
  - (E) COUNTRY: USA
  - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/212,185
  - (B) FILING DATE: 11-MAR-1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/980,498
  - (B) FILING DATE: 23-NOV-1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/854,296
  - (B) FILING DATE: 19-MAR-1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO US93/02569
  - (B) FILING DATE: 19-MAR-1993
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/126,588
  - (B) FILING DATE: 24-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Jackson Esq., David A.
  - (B) REGISTRATION NUMBER: 26,742
  - (C) REFERENCE/DOCKET NUMBER: 600-1-073 CIP
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 201 487-5800
  - (B) TELEFAX: 201 343-1684
  - (C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3268 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 (vi) ORIGINAL SOURCE:  
       (A) ORGANISM: Homo sapiens  
 (vii) IMMEDIATE SOURCE:  
       (B) CLONE: HeLa  
 (ix) FEATURE:  
       (A) NAME/KEY: CDS  
       (B) LOCATION: 25..2577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTGCAACCC TAATCAGAGC CCAA ATG GCG CAG TGG GAA ATG CTG CAG AAT	51
Met Ala Gln Trp Glu Met Leu Gln Asn	
1 5	
CTT GAC AGC CCC TTT CAG GAT CAG CTG CAC CAG CTT TAC TCG CAC AGC	99
Leu Asp Ser Pro Phe Gln Asp Gln Leu His Gln Leu Tyr Ser His Ser	
10 15 20 25	
CTC CTG CCT GTG GAC ATT CGA CAG TAC TTG GCT GTC TGG ATT GAA GAC	147
Leu Leu Pro Val Asp Ile Arg Gln Tyr Leu Ala Val Trp Ile Glu Asp	
30 35 40	
CAG AAC TGG CAG GAA GCT GCA CTT GGG AGT GAT GAT TCC AAG GCT ACC	195
Gln Asn Trp Gln Glu Ala Ala Leu Gly Ser Asp Asp Ser Lys Ala Thr	
45 50 55	
ATG CTA TTC TTC CAC TTC TTG GAT CAG CTG AAC TAT GAG TGT GGC CGT	243
Met Leu Phe Phe His Phe Leu Asp Gln Leu Asn Tyr Glu Cys Gly Arg	
60 65 70	
TGC AGC CAG GAC CCA GAG TCC TTG TTG CTG CAG CAC AAT TTG CGG AAA	291
Cys Ser Gln Asp Pro Glu Ser Leu Leu Leu Gln His Asn Leu Arg Lys	
75 80 85	
TTC TGC CGG GAC ATT CAG CCC TTT TCC CAG GAT CCT ACC CAG TTG GCT	339
Phe Cys Arg Asp Ile Gln Pro Phe Ser Gln Asp Pro Thr Gln Leu Ala	
90 95 100 105	
GAG ATG ATC TTT AAC CTC CTT CTG GAA GAA AAA AGA ATT TTG ATC CAG	387
Glu Met Ile Phe Asn Leu Leu Leu Glu Glu Lys Arg Ile Leu Ile Gln	
110 115 120	
GCT CAG AGG GCC CAA TTG GAA CAA GGA GAG CCA GTT CTC GAA ACA CCT	435
Ala Gln Arg Ala Gln Leu Glu Gln Gly Glu Pro Val Leu Glu Thr Pro	
125 130 135	
GTG GAG AGC CAG CAA CAT GAG ATT GAA TCC CGG ATC CTG GAT TTA AGG	483
Val Glu Ser Gln Gln His Glu Ile Glu Ser Arg Ile Leu Asp Leu Arg	
140 145 150	
GCT ATG ATG GAG AAG CTG GTA AAA TCC ATC AGC CAA CTG AAA GAC CAG	531
Ala Met Met Glu Lys Leu Val Lys Ser Ile Ser Gln Leu Lys Asp Gln	
155 160 165	
CAG GAT GTC TTC TGC TTC CGA TAT AAG ATC CAG GCC AAA GGG AAG ACA	579
Gln Asp Val Phe Cys Phe Arg Tyr Lys Ile Gln Ala Lys Gly Lys Thr	
170 175 180 185	

CCC	TCT	CTG	GAC	CCC	CAT	CAG	ACC	AAA	GAG	CAG	AAG	ATT	CTG	CAG	GAA	627
Pro	Ser	Leu	Asp	Pro	His	Gln	Thr	Lys	Glu	Gln	Lys	Ile	Leu	Gln	Glu	
				190					195					200		
ACT	CTC	AAT	GAA	CTG	GAC	AAA	AGG	AGA	AAG	GAG	GTG	CTG	GAT	GCC	TCC	675
Thr	Leu	Asn	Glu	Leu	Asp	Lys	Arg	Arg	Lys	Glu	Val	Leu	Asp	Ala	Ser	
			205					210					215			
AAA	GCA	CTG	CTA	GGC	CGA	TTA	ACT	ACC	CTA	ATC	GAG	CTA	CTG	CTG	CCA	723
Lys	Ala	Leu	Leu	Gly	Arg	Leu	Thr	Thr	Leu	Ile	Glu	Leu	Leu	Leu	Pro	
		220					225					230				
AAG	TTG	GAG	GAG	TGG	AAG	GCC	CAG	CAG	CAA	AAA	GCC	TGC	ATC	AGA	GCT	771
Lys	Leu	Glu	Glu	Trp	Lys	Ala	Gln	Gln	Gln	Lys	Ala	Cys	Ile	Arg	Ala	
	235					240					245					
CCC	ATT	GAC	CAC	GGG	TTG	GAA	CAG	CTG	GAG	ACA	TGG	TTC	ACA	GCT	GGA	819
Pro	Ile	Asp	His	Gly	Leu	Glu	Gln	Leu	Glu	Thr	Trp	Phe	Thr	Ala	Gly	
250				255						260					265	
GCA	AAG	CTG	TTG	TTT	CAC	CTG	AGG	CAG	CTG	CTG	AAG	GAG	CTG	AAG	GGA	867
Ala	Lys	Leu	Leu	Phe	His	Leu	Arg	Gln	Leu	Leu	Lys	Glu	Leu	Lys	Gly	
				270					275					280		
CTG	AGT	TGC	CTG	GTT	AGC	TAT	CAG	GAT	GAC	CCT	CTG	ACC	AAA	GGG	GTG	915
Leu	Ser	Cys	Leu	Val	Ser	Tyr	Gln	Asp	Asp	Pro	Leu	Thr	Lys	Gly	Val	
			285					290					295			
GAC	CTA	CGC	AAC	GCC	CAG	GTC	ACA	GAG	TTG	CTA	CAG	CGT	CTG	CTC	CAC	963
Asp	Leu	Arg	Asn	Ala	Gln	Val	Thr	Glu	Leu	Leu	Gln	Arg	Leu	Leu	His	
		300					305					310				
AGA	GCC	TTT	GTG	GTA	GAA	ACC	CAG	CCC	TGC	ATG	CCC	CAA	ACT	CCC	CAT	1011
Arg	Ala	Phe	Val	Val	Glu	Thr	Gln	Pro	Cys	Met	Pro	Gln	Thr	Pro	His	
	315					320					325					
CGA	CCC	CTC	ATC	CTC	AAG	ACT	GGC	AGC	AAG	TTC	ACC	GTC	CGA	ACA	AGG	1059
Arg	Pro	Leu	Ile	Leu	Lys	Thr	Gly	Ser	Lys	Phe	Thr	Val	Arg	Thr	Arg	
330					335					340					345	
CTG	CTG	GTG	AGA	CTC	CAG	GAA	GGC	AAT	GAG	TCA	CTG	ACT	GTG	GAA	GTC	1107
Leu	Leu	Val	Arg	Leu	Gln	Glu	Gly	Asn	Glu	Ser	Leu	Thr	Val	Glu	Val	
				350					355					360		
TCC	ATT	GAC	AGG	AAT	CCT	CCT	CAA	TTA	CAA	GGC	TTC	CGG	AAG	TTC	AAC	1155
Ser	Ile	Asp	Arg	Asn	Pro	Pro	Gln	Leu	Gln	Gly	Phe	Arg	Lys	Phe	Asn	
			365					370					375			
ATT	CTG	ACT	TCA	AAC	CAG	AAA	ACT	TTG	ACC	CCC	GAG	AAG	GGG	CAG	AGT	1203
Ile	Leu	Thr	Ser	Asn	Gln	Lys	Thr	Leu	Thr	Pro	Glu	Lys	Gly	Gln	Ser	
		380					385					390				
CAG	GGT	TTG	ATT	TGG	GAC	TTT	GGT	TAC	CTG	ACT	CTG	GTG	GAG	CAA	CGT	1251
Gln	Gly	Leu	Ile	Trp	Asp	Phe	Gly	Tyr	Leu	Thr	Leu	Val	Glu	Gln	Arg	
	395					400					405					
TCA	GGT	GGT	TCA	GGA	AAG	GGC	AGC	AAT	AAG	GGG	CCA	CTA	GGT	GTG	ACA	1299
Ser	Gly	Gly	Ser	Gly	Lys	Gly	Ser	Asn	Lys	Gly	Pro	Leu	Gly	Val	Thr	
410					415					420					425	
GAG	GAA	CTG	CAC	ATC	ATC	AGC	TTC	ACG	GTC	AAA	TAT	ACC	TAC	CAG	GGT	1347
Glu	Glu	Leu	His	Ile	Ile	Ser	Phe	Thr	Val	Lys	Tyr	Thr	Tyr	Gln	Gly	
				430					435					440		
CTG	AAG	CAG	GAG	CTG	AAA	ACG	GAC	ACC	CTC	CCT	GTG	GTG	ATT	ATT	TCC	1395
Leu	Lys	Gln	Glu	Leu	Lys	Thr	Asp	Thr	Leu	Pro	Val	Val	Ile	Ile	Ser	
			445					450					455			

AAC ATG AAC CAG CTC TCA ATT GCC TGG GCT TCA GTT CTC TGG TTC AAT Asn Met Asn Gln Leu Ser Ile Ala Trp Ala Ser Val Leu Trp Phe Asn 460 465 470	1443
TTG CTC AGC CCA AAC CTT CAG AAC CAG CAG TTC TTC TCC AAC CCC CCC Leu Leu Ser Pro Asn Leu Gln Asn Gln Gln Phe Phe Ser Asn Pro Pro 475 480 485	1491
AAG GCC CCC TGG AGC TTG CTG GGC CCT GCT CTC AGT TGG CAG TTC TCC Lys Ala Pro Trp Ser Leu Leu Gly Pro Ala Leu Ser Trp Gln Phe Ser 490 495 500 505	1539
TCC TAT GTT GGC CGA GGC CTC AAC TCA GAC CAG CTG AGC ATG CTG AGA Ser Tyr Val Gly Arg Gly Leu Asn Ser Asp Gln Leu Ser Met Leu Arg 510 515 520	1587
AAC AAG CTG TTC GGG CAG AAC TGT AGG ACT GAG GAT CCA TTA TTG TCC Asn Lys Leu Phe Gly Gln Asn Cys Arg Thr Glu Asp Pro Leu Leu Ser 525 530 535	1635
TGG GCT GAC TTC ACT AAG CGA GAG AGC CCT CCT GGC AAG TTA CCA TTC Trp Ala Asp Phe Thr Lys Arg Glu Ser Pro Pro Gly Lys Leu Pro Phe 540 545 550	1683
TGG ACA TGG CTG GAC AAA ATT CTG GAG TTG GTA CAT GAC CAC CTG AAG Trp Thr Trp Leu Asp Lys Ile Leu Glu Leu Val His Asp His Leu Lys 555 560 565	1731
GAT CTC TGG AAT GAT GGA CGC ATC ATG GGC TTT GTG AGT CGG AGC CAG Asp Leu Trp Asn Asp Gly Arg Ile Met Gly Phe Val Ser Arg Ser Gln 570 575 580 585	1779
GAG CGC CGG CTG CTG AAG AAG ACC ATG TCT GGC ACC TTT CTA CTG CGC Glu Arg Arg Leu Leu Lys Lys Thr Met Ser Gly Thr Phe Leu Leu Arg 590 595 600	1827
TTC AGT GAA TCG TCA GAA GGG GGC ATT ACC TGC TCC TGG GTG GAG CAC Phe Ser Glu Ser Ser Glu Gly Gly Ile Thr Cys Ser Trp Val Glu His 605 610 615	1875
CAG GAT GAT GAC AAG GTG CTC ATC TAC TCT GTG CAA CCG TAC ACG AAG Gln Asp Asp Asp Lys Val Leu Ile Tyr Ser Val Gln Pro Tyr Thr Lys 620 625 630	1923
GAG GTG CTG CAG TCA CTC CCG CTG ACT GAA ATC ATC CGC CAT TAC CAG Glu Val Leu Gln Ser Leu Pro Leu Thr Glu Ile Ile Arg His Tyr Gln 635 640 645	1971
TTG CTC ACT GAG GAG AAT ATA CCT GAA AAC CCA CTG CGC TTC CTC TAT Leu Leu Thr Glu Glu Asn Ile Pro Glu Asn Pro Leu Arg Phe Leu Tyr 650 655 660 665	2019
CCC CGA ATC CCC CGG GAT GAA GCT TTT GGG TGC TAC TAC CAG GAG AAA Pro Arg Ile Pro Arg Asp Glu Ala Phe Gly Cys Tyr Tyr Gln Glu Lys 670 675 680	2067
GTT AAT CTC CAG GAA CGG AGG AAA TAC CTG AAA CAC AGG CTC ATT GTG Val Asn Leu Gln Glu Arg Arg Lys Tyr Leu Lys His Arg Leu Ile Val 685 690 695	2115
GTC TCT AAT AGA CAG GTG GAT GAA CTG CAA CAA CCG CTG GAG CTT AAG Val Ser Asn Arg Gln Val Asp Glu Leu Gln Gln Pro Leu Glu Leu Lys 700 705 710	2163
CCA GAG CCA GAG CTG GAG TCA TTA GAG CTG GAA CTA GGG CTG GTG CCA Pro Glu Pro Glu Leu Glu Ser Leu Glu Leu Glu Leu Gly Leu Val Pro 715 720 725	2211

GAG CCA GAG CTC AGC CTG GAC TTA GAG CCA CTG CTG AAG GCA GGG CTG Glu Pro Glu Leu Ser Leu Asp Leu Glu Pro Leu Leu Lys Ala Gly Leu 730 735 740 745	2259
GAT CTG GGG CCA GAG CTA GAG TCT GTG CTG GAG TCC ACT CTG GAG CCT Asp Leu Gly Pro Glu Leu Glu Ser Val Leu Glu Ser Thr Leu Glu Pro 750 755 760	2307
GTG ATA GAG CCC ACA CTA TGC ATG GTA TCA CAA ACA GTG CCA GAG CCA Val Ile Glu Pro Thr Leu Cys Met Val Ser Gln Thr Val Pro Glu Pro 765 770 775	2355
GAC CAA GGA CCT GTA TCA CAG CCA GTG CCA GAG CCA GAT TTG CCC TGT Asp Gln Gly Pro Val Ser Gln Pro Val Pro Glu Pro Asp Leu Pro Cys 780 785 790	2403
GAT CTG AGA CAT TTG AAC ACT GAG CCA ATG GAA ATC TTC AGA AAC TGT Asp Leu Arg His Leu Asn Thr Glu Pro Met Glu Ile Phe Arg Asn Cys 795 800 805	2451
GTA AAG ATT GAA GAA ATC ATG CCG AAT GGT GAC CCA CTG TTG GCT GGC Val Lys Ile Glu Glu Ile Met Pro Asn Gly Asp Pro Leu Leu Ala Gly 810 815 820 825	2499
CAG AAC ACC GTG GAT GAG GTT TAC GTC TCC CGC CCC AGC CAC TTC TAC Gln Asn Thr Val Asp Glu Val Tyr Val Ser Arg Pro Ser His Phe Tyr 830 835 840	2547
ACT GAT GGA CCC TTG ATG CCT TCT GAC TTC TAGGAACCAC ATTTCTCTCTG Thr Asp Gly Pro Leu Met Pro Ser Asp Phe 845 850	2597
TTCTTTTCAT ATCTCTTTGC CCTTCCTACT CCTCATAGCA TGATATTGTT CTCCAAGGAT	2657
GGGAATCAGG CATGTGTCCC TTCCAAGCTG TGTAACTGT TCAAACCTCAG GCCTGTGTGA	2717
CTCCATTGGG GTGAGAGGTG AAAGCATAAC ATGGGTACAG AGGGGACAAC AATGAATCAG	2777
AACAGATGCT GAGCCATAGG TCTAAATAGG ATCCTGGAGG CTGCCTGCTG TGCTGGGAGG	2837
TATAGGGGTC CTGGGGGCAG GCCAGGGCAG TTGACAGGTA CTTGGAGGGC TCAGGGCAGT	2897
GGCTTCTTTC CAGTATGGAA GGATTTC AAC ATTTTAATAG TTGGTTAGGC TAACTGGTG	2957
CATACTGGCA TTGGCCTTGG TGGGGAGCAC AGACACAGGA TAGGACTCCA TTTCTTTCTT	3017
CCATTCCTTC ATGTCTAGGA TAACTTGCTT TCTTCTTTCC TTTACTCCTG GCTCAAGCCC	3077
TGAATTTCTT CTTTTCTG CAGGGGTTGAG AGCTTTCTGC CTTAGCCTAC CATGTGAAAC	3137
TCTACCCTGA AGAAAGGGAT GGATAGGAAG TAGACCTCTT TTTCTTACCA GTCTCCTCCC	3197
CTACTCTGCC CCCTAAGCTG GCTGTACCTG TTCCTCCCC ATAAAATGAT CCTGCCAATC	3257
TAAAAAAAAA A	3268

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Gln Trp Glu Met Leu Gln Asn Leu Asp Ser Pro Phe Gln Asp  
1 5 10 15  
Gln Leu His Gln Leu Tyr Ser His Ser Leu Leu Pro Val Asp Ile Arg  
20 25 30  
Gln Tyr Leu Ala Val Trp Ile Glu Asp Gln Asn Trp Gln Glu Ala Ala  
35 40 45  
Leu Gly Ser Asp Asp Ser Lys Ala Thr Met Leu Phe Phe His Phe Leu  
50 55 60  
Asp Gln Leu Asn Tyr Glu Cys Gly Arg Cys Ser Gln Asp Pro Glu Ser  
65 70 75 80  
Leu Leu Leu Gln His Asn Leu Arg Lys Phe Cys Arg Asp Ile Gln Pro  
85 90 95  
Phe Ser Gln Asp Pro Thr Gln Leu Ala Glu Met Ile Phe Asn Leu Leu  
100 105 110  
Leu Glu Glu Lys Arg Ile Leu Ile Gln Ala Gln Arg Ala Gln Leu Glu  
115 120 125  
Gln Gly Glu Pro Val Leu Glu Thr Pro Val Glu Ser Gln Gln His Glu  
130 135 140  
Ile Glu Ser Arg Ile Leu Asp Leu Arg Ala Met Met Glu Lys Leu Val  
145 150 155 160  
Lys Ser Ile Ser Gln Leu Lys Asp Gln Gln Asp Val Phe Cys Phe Arg  
165 170 175  
Tyr Lys Ile Gln Ala Lys Gly Lys Thr Pro Ser Leu Asp Pro His Gln  
180 185 190  
Thr Lys Glu Gln Lys Ile Leu Gln Glu Thr Leu Asn Glu Leu Asp Lys  
195 200 205  
Arg Arg Lys Glu Val Leu Asp Ala Ser Lys Ala Leu Leu Gly Arg Leu  
210 215 220  
Thr Thr Leu Ile Glu Leu Leu Leu Pro Lys Leu Glu Glu Trp Lys Ala  
225 230 235 240  
Gln Gln Gln Lys Ala Cys Ile Arg Ala Pro Ile Asp His Gly Leu Glu  
245 250 255  
Gln Leu Glu Thr Trp Phe Thr Ala Gly Ala Lys Leu Leu Phe His Leu  
260 265 270  
Arg Gln Leu Leu Lys Glu Leu Lys Gly Leu Ser Cys Leu Val Ser Tyr  
275 280 285  
Gln Asp Asp Pro Leu Thr Lys Gly Val Asp Leu Arg Asn Ala Gln Val  
290 295 300  
Thr Glu Leu Leu Gln Arg Leu Leu His Arg Ala Phe Val Val Glu Thr  
305 310 315 320  
Gln Pro Cys Met Pro Gln Thr Pro His Arg Pro Leu Ile Leu Lys Thr  
325 330 335  
Gly Ser Lys Phe Thr Val Arg Thr Arg Leu Leu Val Arg Leu Gln Glu  
340 345 350  
Gly Asn Glu Ser Leu Thr Val Glu Val Ser Ile Asp Arg Asn Pro Pro  
355 360 365

Gln Leu Gln Gly Phe Arg Lys Phe Asn Ile Leu Thr Ser Asn Gln Lys  
 370 375 380  
 Thr Leu Thr Pro Glu Lys Gly Gln Ser Gln Gly Leu Ile Trp Asp Phe  
 385 390 395 400  
 Gly Tyr Leu Thr Leu Val Glu Gln Arg Ser Gly Gly Ser Gly Lys Gly  
 405 410 415  
 Ser Asn Lys Gly Pro Leu Gly Val Thr Glu Glu Leu His Ile Ile Ser  
 420 425 430  
 Phe Thr Val Lys Tyr Thr Tyr Gln Gly Leu Lys Gln Glu Leu Lys Thr  
 435 440 445  
 Asp Thr Leu Pro Val Val Ile Ile Ser Asn Met Asn Gln Leu Ser Ile  
 450 455 460  
 Ala Trp Ala Ser Val Leu Trp Phe Asn Leu Leu Ser Pro Asn Leu Gln  
 465 470 475 480  
 Asn Gln Gln Phe Phe Ser Asn Pro Pro Lys Ala Pro Trp Ser Leu Leu  
 485 490 495  
 Gly Pro Ala Leu Ser Trp Gln Phe Ser Ser Tyr Val Gly Arg Gly Leu  
 500 505 510  
 Asn Ser Asp Gln Leu Ser Met Leu Arg Asn Lys Leu Phe Gly Gln Asn  
 515 520 525  
 Cys Arg Thr Glu Asp Pro Leu Leu Ser Trp Ala Asp Phe Thr Lys Arg  
 530 535 540  
 Glu Ser Pro Pro Gly Lys Leu Pro Phe Trp Thr Trp Leu Asp Lys Ile  
 545 550 555 560  
 Leu Glu Leu Val His Asp His Leu Lys Asp Leu Trp Asn Asp Gly Arg  
 565 570 575  
 Ile Met Gly Phe Val Ser Arg Ser Gln Glu Arg Arg Leu Leu Lys Lys  
 580 585 590  
 Thr Met Ser Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Glu Gly  
 595 600 605  
 Gly Ile Thr Cys Ser Trp Val Glu His Gln Asp Asp Asp Lys Val Leu  
 610 615 620  
 Ile Tyr Ser Val Gln Pro Tyr Thr Lys Glu Val Leu Gln Ser Leu Pro  
 625 630 635 640  
 Leu Thr Glu Ile Ile Arg His Tyr Gln Leu Leu Thr Glu Glu Asn Ile  
 645 650 655  
 Pro Glu Asn Pro Leu Arg Phe Leu Tyr Pro Arg Ile Pro Arg Asp Glu  
 660 665 670  
 Ala Phe Gly Cys Tyr Tyr Gln Glu Lys Val Asn Leu Gln Glu Arg Arg  
 675 680 685  
 Lys Tyr Leu Lys His Arg Leu Ile Val Val Ser Asn Arg Gln Val Asp  
 690 695 700  
 Glu Leu Gln Gln Pro Leu Glu Leu Lys Pro Glu Pro Glu Leu Glu Ser  
 705 710 715 720  
 Leu Glu Leu Glu Leu Gly Leu Val Pro Glu Pro Glu Leu Ser Leu Asp  
 725 730 735

Leu Glu Pro Leu Leu Lys Ala Gly Leu Asp Leu Gly Pro Glu Leu Glu  
 740 745 750  
 Ser Val Leu Glu Ser Thr Leu Glu Pro Val Ile Glu Pro Thr Leu Cys  
 755 760 765  
 Met Val Ser Gln Thr Val Pro Glu Pro Asp Gln Gly Pro Val Ser Gln  
 770 775 780  
 Pro Val Pro Glu Pro Asp Leu Pro Cys Asp Leu Arg His Leu Asn Thr  
 785 790 795 800  
 Glu Pro Met Glu Ile Phe Arg Asn Cys Val Lys Ile Glu Glu Ile Met  
 805 810 815  
 Pro Asn Gly Asp Pro Leu Leu Ala Gly Gln Asn Thr Val Asp Glu Val  
 820 825 830  
 Tyr Val Ser Arg Pro Ser His Phe Tyr Thr Asp Gly Pro Leu Met Pro  
 835 840 845  
 Ser Asp Phe  
 850

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3943 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Human Stat91

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 197..2449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTAAACCTC TCGCCGAGCC CCTCCGCAGA CTCTGCGCCG GAAAGTTTCA TTTGCTGTAT	60
GCCATCCTCG AGAGCTGTCT AGGTAAACGT TCGCACTCTG TGTATATAAC CTCGACAGTC	120
TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTTGGTTG AATCCCCAGG CCCTTGTTGG	180
GGCACAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC	229
Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp	
1 5 10	
TCA AAA TTC CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC	277
Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro	
15 20 25	
ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG	325
Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp	
30 35 40	



GAG CAC GCT GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp 45 50 55	373
CTC CTG TCA CAG CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn 60 65 70 75	421
AAC TTC TTG CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln 80 85 90	469
GAT AAT TTT CAG GAA GAC CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser 95 100 105	517
TGT CTG AAG GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn 110 115 120	565
CAG GCT CAG TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln 125 130 135	613
AAA GAG CTT GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys 140 145 150 155	661
ATA GAG CAT GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp 160 165 170	709
TTC AAA TGC AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val 175 180 185	757
GCA AAG AGT GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr 190 195 200	805
TTA ATG CTT GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu 205 210 215	853
TTG CTG AAT GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu 220 225 230 235	901
CTA GTG GAG TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro 240 245 250	949
CCC AAT GCT TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala 255 260 265	997
GAG AGT CTG CAG CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu 270 275 280	1045
GAA CAG AAA TAC ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln 285 290 295	1093
GTG TTA TGG GAC CGC ACC TTC AGT CTT TTC CAG CAG CTC ATT CAG AGC Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser 300 305 310 315	1141

TCG TTT GTG GTG GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG	1189
Ser Phe Val Val Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg	
320 325 330	
CCG CTG GTC TTG AAG ACA GGG GTC CAG TTC ACT GTG AAG TTG AGA CTG	1237
Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu	
335 340 345	
TTG GTG AAA TTG CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA	1285
Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu	
350 355 360	
TTT GAT AAA GAT GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG	1333
Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys	
365 370 375	
TTC AAC ATT TTG GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC	1381
Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser	
380 385 390 395	
ACC AAT GGC AGT CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA	1429
Thr Asn Gly Ser Leu Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu	
400 405 410	
CAG AAA AAT GCT GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT	1477
Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr	
415 420 425	
GAA GAG CTT CAC TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT	1525
Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly	
430 435 440	
TTG GTA ATT GAC CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC	1573
Leu Val Ile Asp Leu Glu Thr Ser Leu Pro Val Val Ile Ser	
445 450 455	
AAC GTC AGC CAG CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC	1621
Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn	
460 465 470 475	
ATG CTG GTG GCG GAA CCC AGG AAT CTG TCC TTC TTC CTG ACT CCA CCA	1669
Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro	
480 485 490	
TGT GCA CGA TGG GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT	1717
Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser	
495 500 505	
TCT GTC ACC AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA	1765
Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly	
510 515 520	
GAG AAG CTT CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG	1813
Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp	
525 530 535	
ACG AGG TTT TGT AAG GAA AAT ATA AAT GAT AAA AAT TTT CCC TTC TGG	1861
Thr Arg Phe Cys Lys Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp	
540 545 550 555	
CTT TGG ATT GAA AGC ATC CTA GAA CTC ATT AAA AAA CAC CTG CTC CCT	1909
Leu Trp Ile Glu Ser Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro	
560 565 570	
CTC TGG AAT GAT GGG TGC ATC ATG GGC TTC ATC AGC AAG GAG CGA GAG	1957
Leu Trp Asn Asp Gly Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu	
575 580 585	

CGT GCC CTG TTG AAG GAC CAG CAG CCG GGG ACC TTC CTG CTG CGG TTC Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe 590 595 600	2005
AGT GAG AGC TCC CGG GAA GGG GCC ATC ACA TTC ACA TGG GTG GAG CGG Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg 605 610 615	2053
TCC CAG AAC GGA GGC GAA CCT GAC TTC CAT GCG GTT GAA CCC TAC ACG Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr 620 625 630 635	2101
AAG AAA GAA CTT TCT GCT GTT ACT TTC CCT GAC ATC ATT CGC AAT TAC Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr 640 645 650	2149
AAA GTC ATG GCT GCT GAG AAT ATT CCT GAG AAT CCC CTG AAG TAT CTG Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu 655 660 665	2197
TAT CCA AAT ATT GAC AAA GAC CAT GCC TTT GGA AAG TAT TAC TCC AGG Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg 670 675 680	2245
CCA AAG GAA GCA CCA GAG CCA ATG GAA CTT GAT GGC CCT AAA GGA ACT Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr 685 690 695	2293
GGA TAT ATC AAG ACT GAG TTG ATT TCT GTG TCT GAA GTT CAC CCT TCT Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val Ser Glu Val His Pro Ser 700 705 710 715	2341
AGA CTT CAG ACC ACA GAC AAC CTG CTC CCC ATG TCT CCT GAG GAG TTT Arg Leu Gln Thr Thr Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe 720 725 730	2389
GAC GAG GTG TCT CGG ATA GTG GGC TCT GTA GAA TTC GAC AGT ATG ATG Asp Glu Val Ser Arg Ile Val Gly Ser Val Glu Phe Asp Ser Met Met 735 740 745	2437
AAC ACA GTA TAGAGCATGA ATTTTTTTTCA TCTTCTCTGG CGACAGTTTT Asn Thr Val 750	2486
CCTTCTCATC TGTGATTCCC TCCTGCTACT CTGTTCTTC ACATCCTGTG TTTCTAGGGA	2546
AATGAAAGAA AGGCCAGCAA ATTCGCTGCA ACCTGTTGAT AGCAAGTGAA TTTTTCTCTA	2606
ACTCAGAAAC ATCAGTTACT CTGAAGGGCA TCATGCATCT TACTGAAGGT AAAATTGAAA	2666
GGCATTCTCT GAAGAGTGGG TTTACAAAGT GAAAAACATC CAGATACACC CAAAGTATCA	2726
GGACGAGAAT GAGGGTCCTT TGGGAAAGGA GAAGTTAAGC AACATCTAGC AAATGTTATG	2786
CATAAAGTCA GTGCCCAACT GTTATAGGTT GTTGGATAAA TCAGTGGTTA TTTAGGGAAC	2846
TGCTTGACGT AGGAACGGTA AATTTCTGTG GGAGAATTCT TACATGTTTT CTTTGCTTTA	2906
AGTGTAAGTG GCAGTTTTCC ATTGGTTTAC CTGTGAAATA GTTCAAAGCC AAGTTTATAT	2966
ACAATTATAT CAGTCCTCTT TCAAAGGTAG CCATCATGGA TCTGGTAGGG GGAAAATGTG	3026
TATTTTATTA CATCTTTCAC ATTGGCTATT TAAAGACAAA GACAAATTCT GTTTCTTGAG	3086
AAGAGAACAT TTCCAAATTC ACAAGTTGTG TTTGATATCC AAAGCTGAAT ACATTCTGCT	3146
TTCATCTTGG TCACATACAA TTATTTTTAC AGTTCTCCCA AGGGAGTTAG GCTATTCACA	3206
ACCACTCATT CAAAAGTTGA AATTAACCAT AGATGTAGAT AAACCTCAGAA ATTTAATTCA	3266

TGTTTCTTAA ATGGGCTACT TTGTCCTTTT TGTTATTAGG GTGGTATTTA GTCTATTAGC	3326
CACAAAATTG GGAAAGGAGT AGAAAAAGCA GTAACGTACA ACTTGAATAA TACACCAGAG	3386
ATAATATGAG AATCAGATCA TTTCAAAACT CATTTCTTAT GTAACGTGCAT TGAGAACTGC	3446
ATATGTTTTG CTGATATATG TGTTTTTCAC ATTTGCGAAT GGTTCATTTC TCTCTCCTGT	3506
ACTTTTTCCA GACACTTTTT TGAGTGGATG ATGTTTCGTG AAGTATACTG TATTTTTACC	3566
TTTTTCCTTC CTTATCACTG ACACAAAAAG TAGATTAAGA GATGGGTTTG ACAAGGTTCT	3626
TCCCTTTTAC ATACTGCTGT CTATGTGGCT GTATCTTGTT TTTCCACTAC TGCTACCACA	3686
ACTATATTAT CATGCAAATG CTGTATTCTT CTTTGGTGGA GATAAAGATT TCTTGAGTTT	3746
TGTTTTAAAA TTAAAGCTAA AGTATCTGTA TTGCATTAAA TATAATATCG ACACAGTGCT	3806
TTCCGTGGCA CTGCATACAA TCTGAGGCCT CCTCTCTCAG TTTTATATA GATGGCGAGA	3866
ACCTAAGTTT CAGTTGATTT TACAATTGAA ATGACTAAAA AACAAAGAAG ACAACATTAA	3926
AAACAATAAT GTTTCTA	3943

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 750 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Gln	Trp	Tyr	Glu	Leu	Gln	Gln	Leu	Asp	Ser	Lys	Phe	Leu	Glu	1	5	10	15
Gln	Val	His	Gln	Leu	Tyr	Asp	Asp	Ser	Phe	Pro	Met	Glu	Ile	Arg	Gln	20	25	30	
Tyr	Leu	Ala	Gln	Trp	Leu	Glu	Lys	Gln	Asp	Trp	Glu	His	Ala	Ala	Asn	35	40	45	
Asp	Val	Ser	Phe	Ala	Thr	Ile	Arg	Phe	His	Asp	Leu	Leu	Ser	Gln	Leu	50	55	60	
Asp	Asp	Gln	Tyr	Ser	Arg	Phe	Ser	Leu	Glu	Asn	Asn	Phe	Leu	Leu	Gln	65	70	75	80
His	Asn	Ile	Arg	Lys	Ser	Lys	Arg	Asn	Leu	Gln	Asp	Asn	Phe	Gln	Glu	85	90	95	
Asp	Pro	Ile	Gln	Met	Ser	Met	Ile	Ile	Tyr	Ser	Cys	Leu	Lys	Glu	Glu	100	105	110	
Arg	Lys	Ile	Leu	Glu	Asn	Ala	Gln	Arg	Phe	Asn	Gln	Ala	Gln	Ser	Gly	115	120	125	
Asn	Ile	Gln	Ser	Thr	Val	Met	Leu	Asp	Lys	Gln	Lys	Glu	Leu	Asp	Ser	130	135	140	
Lys	Val	Arg	Asn	Val	Lys	Asp	Lys	Val	Met	Cys	Ile	Glu	His	Glu	Ile	145	150	155	160
Lys	Ser	Leu	Glu	Asp	Leu	Gln	Asp	Glu	Tyr	Asp	Phe	Lys	Cys	Lys	Thr	165	170	175	

Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln  
 180 185 190  
 Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn  
 195 200 205  
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr  
 210 215 220  
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys  
 225 230 235 240  
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu  
 245 250 255  
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln  
 260 265 270  
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr  
 275 280 285  
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg  
 290 295 300  
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu  
 305 310 315 320  
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys  
 325 330 335  
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln  
 340 345 350  
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val  
 355 360 365  
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly  
 370 375 380  
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu  
 385 390 395 400  
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly  
 405 410 415  
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser  
 420 425 430  
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu  
 435 440 445  
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu  
 450 455 460  
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu  
 465 470 475 480  
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala  
 485 490 495  
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg  
 500 505 510  
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly  
 515 520 525  
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys  
 530 535 540

Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser  
 545 550 555 560  
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly  
 565 570 575  
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys  
 580 585 590  
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg  
 595 600 605  
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly  
 610 615 620  
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser  
 625 630 635 640  
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala  
 645 650 655  
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp  
 660 665 670  
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro  
 675 680 685  
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr  
 690 695 700  
 Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr  
 705 710 715 720  
 Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg  
 725 730 735  
 Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val  
 740 745 750

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2607 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 197..2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTAAACCTC TCGCCGAGCC CCTCCGCAGA CTCTGCGCCG GAAAGTTTCA TTTGCTGTAT	60
GCCATCCTCG AGAGCTGTCT AGGTAAACGT TCGCACTCTG TGTATATAAC CTCGACAGTC	120
TTGGCACCTA ACGTGCTGTG CGTAGCTGCT CCTTTGGTTG AATCCCCAGG CCCTTGTTGG	180

GGCACAAAGGT GGCAGG ATG TCT CAG TGG TAC GAA CTT CAG CAG CTT GAC	229
Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp	
1 5 10	
TCA AAA TTC CTG GAG CAG GTT CAC CAG CTT TAT GAT GAC AGT TTT CCC	277
Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro	
15 20 25	
ATG GAA ATC AGA CAG TAC CTG GCA CAG TGG TTA GAA AAG CAA GAC TGG	325
Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp	
30 35 40	
GAG CAC GCT GCC AAT GAT GTT TCA TTT GCC ACC ATC CGT TTT CAT GAC	373
Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp	
45 50 55	
CTC CTG TCA CAG CTG GAT GAT CAA TAT AGT CGC TTT TCT TTG GAG AAT	421
Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn	
60 65 70 75	
AAC TTC TTG CTA CAG CAT AAC ATA AGG AAA AGC AAG CGT AAT CTT CAG	469
Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln	
80 85 90	
GAT AAT TTT CAG GAA GAG CCA ATC CAG ATG TCT ATG ATC ATT TAC AGC	517
Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser	
95 100 105	
TGT CTG AAG GAA GAA AGG AAA ATT CTG GAA AAC GCC CAG AGA TTT AAT	565
Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn	
110 115 120	
CAG GCT CAG TCG GGG AAT ATT CAG AGC ACA GTG ATG TTA GAC AAA CAG	613
Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln	
125 130 135	
AAA GAG CTT GAC AGT AAA GTC AGA AAT GTG AAG GAC AAG GTT ATG TGT	661
Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys Val Met Cys	
140 145 150 155	
ATA GAG CAT GAA ATC AAG AGC CTG GAA GAT TTA CAA GAT GAA TAT GAC	709
Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp	
160 165 170	
TTC AAA TGC AAA ACC TTG CAG AAC AGA GAA CAC GAG ACC AAT GGT GTG	757
Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val	
175 180 185	
GCA AAG AGT GAT CAG AAA CAA GAA CAG CTG TTA CTC AAG AAG ATG TAT	805
Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr	
190 195 200	
TTA ATG CTT GAC AAT AAG AGA AAG GAA GTA GTT CAC AAA ATA ATA GAG	853
Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys Ile Ile Glu	
205 210 215	
TTG CTG AAT GTC ACT GAA CTT ACC CAG AAT GCC CTG ATT AAT GAT GAA	901
Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu	
220 225 230 235	
CTA GTG GAG TGG AAG CGG AGA CAG CAG AGC GCC TGT ATT GGG GGG CCG	949
Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro	
240 245 250	
CCC AAT GCT TGC TTG GAT CAG CTG CAG AAC TGG TTC ACT ATA GTT GCG	997
Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala	
255 260 265	
GAG AGT CTG CAG CAA GTT CGG CAG CAG CTT AAA AAG TTG GAG GAA TTG	1045

Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu	
270 275 280	
GAA CAG AAA TAC ACC TAC GAA CAT GAC CCT ATC ACA AAA AAC AAA CAA	1093
Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln	
285 290 295	
GTG TTA TGG GAC CGC ACC TTC AGT CTT TTC CAG CAG CTC ATT CAG AGC	1141
Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser	
300 305 310 315	
TCG TTT GTG GTG GAA AGA CAG CCC TGC ATG CCA ACG CAC CCT CAG AGG	1189
Ser Phe Val Val Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg	
320 325 330	
CCG CTG GTC TTG AAG ACA GGG GTC CAG TTC ACT GTG AAG TTG AGA CTG	1237
Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu	
335 340 345	
TTG GTG AAA TTG CAA GAG CTG AAT TAT AAT TTG AAA GTC AAA GTC TTA	1285
Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu	
350 355 360	
TTT GAT AAA GAT GTG AAT GAG AGA AAT ACA GTA AAA GGA TTT AGG AAG	1333
Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys	
365 370 375	
TTC AAC ATT TTG GGC ACG CAC ACA AAA GTG ATG AAC ATG GAG GAG TCC	1381
Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser	
380 385 390 395	
ACC AAT GGC AGT CTG GCG GCT GAA TTT CGG CAC CTG CAA TTG AAA GAA	1429
Thr Asn Gly Ser Leu Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu	
400 405 410	
CAG AAA AAT GCT GGC ACC AGA ACG AAT GAG GGT CCT CTC ATC GTT ACT	1477
Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr	
415 420 425	
GAA GAG CTT CAC TCC CTT AGT TTT GAA ACC CAA TTG TGC CAG CCT GGT	1525
Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly	
430 435 440	
TTG GTA ATT GAC CTC GAG ACG ACC TCT CTG CCC GTT GTG GTG ATC TCC	1573
Leu Val Ile Asp Leu Glu Thr Ser Leu Pro Val Val Val Ile Ser	
445 450 455	
AAC GTC AGC CAG CTC CCG AGC GGT TGG GCC TCC ATC CTT TGG TAC AAC	1621
Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn	
460 465 470 475	
ATG CTG GTG GCG GAA CCC AGG AAT CTG TCC TTC TTC CTG ACT CCA CCA	1669
Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro	
480 485 490	
TGT GCA CGA TGG GCT CAG CTT TCA GAA GTG CTG AGT TGG CAG TTT TCT	1717
Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser	
495 500 505	
TCT GTC ACC AAA AGA GGT CTC AAT GTG GAC CAG CTG AAC ATG TTG GGA	1765
Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly	
510 515 520	
GAG AAG CTT CTT GGT CCT AAC GCC AGC CCC GAT GGT CTC ATT CCG TGG	1813
Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp	
525 530 535	



ACG Thr 540	AGG Arg	TTT Phe	TGT Cys	AAG Lys	GAA Glu 545	AAT Asn	ATA Ile	AAT Asn	GAT Asp	AAA Lys 550	AAT Asn	TTT Phe	CCC Pro	TTC Phe	TGG Trp 555	1861
CTT Leu	TGG Trp	ATT Ile	GAA Glu	AGC Ser 560	ATC Ile	CTA Leu	GAA Glu	CTC Leu	ATT Ile 565	AAA Lys	AAA Lys	CAC His	CTG Leu	CTC Leu	CCT Pro 570	1909
CTC Leu	TGG Trp	AAT Asn	GAT Asp 575	GGG Gly	TGC Cys	ATC Ile	ATG Met	GGC Gly 580	TTC Phe	ATC Ile	AGC Ser	AAG Lys	GAG Glu 585	CGA Arg	GAG Glu	1957
CGT Arg	GCC Ala	CTG Leu 590	TTG Leu	AAG Lys	GAC Asp	CAG Gln	CAG Gln 595	CCG Pro	GGG Gly	ACC Thr	TTC Phe	CTG Leu 600	CTG Leu	CGG Arg	TTC Phe	2005
AGT Ser	GAG Glu 605	AGC Ser	TCC Ser	CGG Arg	GAA Glu	GGG Gly 610	GCC Ala	ATC Ile	ACA Thr	TTC Phe	ACA Thr 615	TGG Trp	GTG Val	GAG Glu	CGG Arg	2053
TCC Ser 620	CAG Gln	AAC Asn	GGA Gly	GGC Gly	GAA Glu 625	CCT Pro	GAC Asp	TTC Phe	CAT His	GCG Ala 630	GTT Val	GAA Glu	CCC Pro	TAC Tyr	ACG Thr 635	2101
AAG Lys	AAA Lys	GAA Glu	CTT Leu	TCT Ser 640	GCT Ala	GTT Val	ACT Thr	TTC Phe	CCT Pro 645	GAC Asp	ATC Ile	ATT Ile	CGC Arg	AAT Asn 650	TAC Tyr	2149
AAA Lys	GTC Val	ATG Met	GCT Ala 655	GCT Ala	GAG Glu	AAT Asn	ATT Ile	CCT Pro 660	GAG Glu	AAT Asn	CCC Pro	CTG Leu	AAG Lys 665	TAT Tyr	CTG Leu	2197
TAT Tyr	CCA Pro	AAT Asn 670	ATT Ile	GAC Asp	AAA Lys	GAC Asp	CAT His 675	GCC Ala	TTT Phe	GGA Gly	AAG Lys	TAT Tyr 680	TAC Tyr	TCC Ser	AGG Arg	2245
CCA Pro 685	AAG Lys	GAA Glu	GCA Ala	CCA Pro	GAG Glu	CCA Pro	ATG Met 690	GAA Glu	CTT Leu	GAT Asp	GGC Gly 695	CCT Pro	AAA Lys	GGA Gly	ACT Thr	2293
GGA Gly 700	TAT Tyr	ATC Ile	AAG Lys	ACT Thr	GAG Glu 705	TTG Leu	ATT Ile	TCT Ser	GTG Val	TCT Ser 710	GAA Glu	GTG Val	TAAGTGAACA			2342
CAGAAGAGTG	ACATGTTTAC	AAACCTCAAG	CCAGCCTTGC	TCCTGGCTGG	GGCCTGTTGA											2402
AGATGCTTGT	ATTTTACTTT	TCCATTGTAA	TTGCTATCGC	CATCACAGCT	GAAGTTGTTG											2462
AGATCCCCGT	GTTACTGCCT	ATCAGCATTT	TACTACTTTA	AAAAAAAAAA	AAAAAGCCAA											2522
AAACCAAATT	TGTATTTAAG	GTATATAAAT	TTTCCCAAAA	CTGATACCCT	TTGAAAAAGT											2582
ATAAATAAAA	TGAGCAAAAAG	TTGAA														2607

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Gln	Trp	Tyr	Glu	Leu	Gln	Gln	Leu	Asp	Ser	Lys	Phe	Leu	Glu
1				5					10					15	

Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln  
 20 25 30  
 Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn  
 35 40 45  
 Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Ser Gln Leu  
 50 55 60  
 Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln  
 65 70 75 80  
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu  
 85 90 95  
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu  
 100 105 110  
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly  
 115 120 125  
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser  
 130 135 140  
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile  
 145 150 155 160  
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr  
 165 170 175  
 Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln  
 180 185 190  
 Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn  
 195 200 205  
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr  
 210 215 220  
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys  
 225 230 235 240  
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu  
 245 250 255  
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln  
 260 265 270  
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr  
 275 280 285  
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg  
 290 295 300  
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu  
 305 310 315 320  
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys  
 325 330 335  
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln  
 340 345 350  
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val  
 355 360 365  
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly  
 370 375 380

Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu  
 385 390 395 400  
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly  
 405 410 415  
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser  
 420 425 430  
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu  
 435 440 445  
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu  
 450 455 460  
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu  
 465 470 475 480  
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala  
 485 490 495  
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg  
 500 505 510  
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly  
 515 520 525  
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys  
 530 535 540  
 Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser  
 545 550 555 560  
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly  
 565 570 575  
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys  
 580 585 590  
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg  
 595 600 605  
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly  
 610 615 620  
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser  
 625 630 635 640  
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala  
 645 650 655  
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp  
 660 665 670  
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro  
 675 680 685  
 Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr  
 690 695 700  
 Glu Leu Ile Ser Val Ser Glu Val  
 705 710

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2277 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:

(B) CLONE: Murine Stat91

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 5..2251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGG ATG TCA CAG TGG TTC GAG CTT CAG CAG CTG GAC TCC AAG TTC CTG	49
Met Ser Gln Trp Phe Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu	
1 5 10 15	
GAG CAG GTC CAC CAG CTG TAC GAT GAC AGT TTC CCC ATG GAA ATC AGA	97
Glu Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg	
20 25 30	
CAG TAC CTG GCC CAG TGG CTG GAA AAG CAA GAC TGG GAG CAC GCT GCC	145
Gln Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala	
35 40 45	
TAT GAT GTC TCG TTT GCG ACC ATC CGC TTC CAT GAC CTC CTC TCA CAG	193
Tyr Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln	
50 55 60	
CTG GAC GAC CAG TAC AGC CGC TTT TCT CTG GAG AAT AAT TTC TTG TTG	241
Leu Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu	
65 70 75	
CAG CAC AAC ATA CGG AAA AGC AAG CGT AAT CTC CAG GAT AAC TTC CAA	289
Gln His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln	
80 85 90 95	
GAA GAT CCC GTA CAG ATG TCC ATG ATC ATC TAC AAC TGT CTG AAG GAA	337
Glu Asp Pro Val Gln Met Ser Met Ile Ile Tyr Asn Cys Leu Lys Glu	
100 105 110	
GAA AGG AAG ATT TTG GAA AAT GCC CAA AGA TTT AAT CAG GCC CAG GAG	385
Glu Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Glu	
115 120 125	
GGA AAT ATT CAG AAC ACT GTG ATG TTA GAT AAA CAG AAG GAG CTG GAC	433
Gly Asn Ile Gln Asn Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp	
130 135 140	
AGT AAA GTC AGA AAT GTG AAG GAT CAA GTC ATG TGC ATA GAG CAG GAA	481
Ser Lys Val Arg Asn Val Lys Asp Gln Val Met Cys Ile Glu Gln Glu	
145 150 155	
ATC AAG ACC CTA GAA GAA TTA CAA GAT GAA TAT GAC TTT AAA TGC AAA	529
Ile Lys Thr Leu Glu Glu Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys	
160 165 170 175	
ACC TCT CAG AAC AGA GAA GGT GAA GCC AAT GGT GTG GCG AAG AGC GAC	577
Thr Ser Gln Asn Arg Glu Gly Glu Ala Asn Gly Val Ala Lys Ser Asp	
180 185 190	

CAA AAA CAG GAA CAG CTG CTG CTC CAC AAG ATG TTT TTA ATG CTT GAC Gln Lys Gln Glu Gln Leu Leu Leu His Lys Met Phe Leu Met Leu Asp 195 200 205	625
AAT AAG AGA AAG GAG ATA ATT CAC AAA ATC AGA GAG TTG CTG AAT TCC Asn Lys Arg Lys Glu Ile Ile His Lys Ile Arg Glu Leu Leu Asn Ser 210 215 220	673
ATC GAG CTC ACT CAG AAC ACT CTG ATT AAT GAC GAG CTC GTG GAG TGG Ile Glu Leu Thr Gln Asn Thr Leu Ile Asn Asp Glu Leu Val Glu Trp 225 230 235	721
AAG CGA AGG CAG CAG AGC GCC TGC ATC GGG GGA CCG CCC AAC GCC TGC Lys Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys 240 245 255	769
CTG GAT CAG CTG CAA ACG TGG TTC ACC ATT GTT GCA GAG ACC CTG CAG Leu Asp Gln Leu Gln Thr Trp Phe Thr Ile Val Ala Glu Thr Leu Gln 260 265 270	817
CAG ATC CGT CAG CAG CTT AAA AAG CTG GAG GAG TTG GAA CAG AAA TTC Gln Ile Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Phe 275 280 285	865
ACC TAT GAG CCC GAC CCT ATT ACA AAA AAC AAG CAG GTG TTG TCA GAT Thr Tyr Glu Pro Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Ser Asp 290 295 300	913
CGA ACC TTC CTC CTC TTC CAG CAG CTC ATT CAG AGC TCC TTC GTG GTA Arg Thr Phe Leu Leu Phe Gln Gln Leu Ile Gln Ser Phe Val Val 305 310 315	961
GAA CGA CAG CCG TGC ATG CCC ACT CAC CCG CAG AGG CCC CTG GTC TTG Glu Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu 320 325 330 335	1009
AAG ACT GGG GTA CAG TTC ACT GTC AAG TCG AGA CTG TTG GTG AAA TTG Lys Thr Gly Val Gln Phe Thr Val Lys Ser Arg Leu Leu Val Lys Leu 340 345 350	1057
CAA GAG TCG AAT CTA TTA ACG AAA GTG AAA TGT CAC TTT GAC AAA GAT Gln Glu Ser Asn Leu Leu Thr Lys Val Lys Cys His Phe Asp Lys Asp 355 360 365	1105
GTG AAC GAG AAA AAC ACA GTT AAA GGA TTT CGG AAG TTC AAC ATC TTG Val Asn Glu Lys Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu 370 375 380	1153
GGT ACG CAC ACA AAA GTG ATG AAC ATG GAA GAA TCC ACC AAC GGA AGT Gly Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser 385 390 395	1201
CTG GCA GCT GAG CTC CGA CAC CTG CAA CTG AAG GAA CAG AAA AAC GCT Leu Ala Ala Glu Leu Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala 400 405 410 415	1249
GGG AAC AGA ACT AAT GAG GGG CCT CTC ATT GTC ACC GAA GAA CTT CAC Gly Asn Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His 420 425 430	1297
TCT CTT AGC TTT GAA ACC CAG TTG TGC CAG CCA GGC TTG GTG ATT GAC Ser Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp 435 440 445	1345
CTG GAG ACC ACC TCT CTT CCT GTC GTG GTG ATC TCC AAC GTC AGC CAG Leu Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln 450 455 460	1393

CTC Leu	CCC Pro 465	AGT Ser	GGC Gly	TGG Trp	GCG Ala	TCT Ser 470	ATC Ile	CTG Leu	TGG Trp	TAC Tyr	AAC Asn 475	ATG Met	CTG Leu	GTG Val	ACA Thr	1441
GAG Glu 480	CCC Pro	AGG Arg	AAT Asn	CTC Leu	TCC Ser 485	TTC Phe	TTC Phe	CTG Leu	AAC Asn	CCC Pro 490	CCG Pro	TGC Cys	GCG Ala	TGG Trp 495	TGG Trp	1489
TCC Ser	CAG Gln	CTC Leu	TCA Ser	GAG Glu 500	GTG Val	TTG Leu	AGT Ser	TGG Trp	CAG Gln 505	TTT Phe	TCA Ser	TCA Ser	GTC Val 510	ACC Thr	AAG Lys	1537
AGA Arg	GGT Gly	CTG Leu	AAC Asn 515	GCA Ala	GAC Asp	CAG Gln	CTG Leu	AGC Ser 520	ATG Met	CTG Leu	GGA Gly	GAG Glu	AAG Lys 525	CTG Leu	CTG Leu	1585
GGC Gly	CCT Pro 530	AAT Asn	GCT Ala	GGC Gly	CCT Pro	GAT Asp	GGT Gly 535	CTT Leu	ATT Ile	CCA Pro	TGG Trp	ACA Thr 540	AGG Arg	TTT Phe	TGT Cys	1633
AAG Lys	GAA Glu 545	AAT Asn	ATT Ile	AAT Asn	GAT Asp	AAA Lys 550	AAT Asn	TTC Phe	TCC Ser	TTC Phe	TGG Trp 555	CCT Pro	TGG Trp	ATT Ile	GAC Asp	1681
ACC Thr 560	ATC Ile	CTA Leu	GAG Glu	CTC Leu	ATT Ile 565	AAG Lys	AAC Asn	GAC Asp	CTG Leu	CTG Leu 570	TGC Cys	CTC Leu	TGG Trp	AAT Asn	GAT Asp 575	1729
GGG Gly	TGC Cys	ATT Ile	ATG Met	GGC Gly 580	TTC Phe	ATC Ile	AGC Ser	AAG Lys	GAG Glu 585	CGA Arg	GAA Glu	CGC Arg	GCT Ala	CTG Leu 590	CTC Leu	1777
AAG Lys	GAC Asp	CAG Gln	CAG Gln 595	CCA Pro	GGG Gly	ACG Thr	TTC Phe	CTG Leu 600	CTT Leu	AGA Arg	TTC Phe	AGT Ser 605	GAG Glu 605	AGC Ser	TCC Ser	1825
CGG Arg	GAA Glu	GGG Gly	GCC Ala 610	ATC Ile	ACA Thr	TTC Phe 615	ACA Thr	TGG Trp	GTG Val	GAA Glu	CGG Arg	TCC Ser 620	CAG Gln	AAC Asn	GGA Gly	1873
GGT Gly 625	GAA Glu	CCT Pro	GAC Asp	TTC Phe	CAT His	GCC Ala 630	GTG Val	GAG Glu	CCC Pro	TAC Tyr	ACG Thr 635	AAA Lys	AAA Lys	GAA Glu	CTT Leu	1921
TCA Ser 640	GCT Ala	GTT Val	ACT Thr	TTC Phe	CCA Pro 645	GAT Asp	ATT Ile	ATT Ile	CGC Arg	AAC Asn 650	TAC Tyr	AAA Lys	GTC Val	ATG Met	GCT Ala 655	1969
GCC Ala	GAG Glu	AAC Asn	ATA Ile 660	CCA Pro	GAG Glu	AAT Asn	CCC Pro	CTG Leu	AAG Lys 665	TAT Tyr	CTG Leu	TAC Tyr	CCC Pro	AAT Asn 670	ATT Ile	2017
GAC Asp	AAA Lys	GAC Asp	CAC His 675	GCC Ala	TTT Phe	GGG Gly	AAG Lys 680	TAT Tyr	TAT Tyr	TCC Ser	AGA Arg	CCA Pro	AAG Lys 685	GAA Glu	GCA Ala	2065
CCA Pro	GAA Glu 690	CCG Pro	ATG Met	GAG Glu	CTT Leu	GAC Asp	GAC Asp 695	CCT Pro	AAG Lys	CGA Arg	ACT Thr	GGA Gly 700	TAC Tyr	ATC Ile	AAG Lys	2113
ACT Thr 705	GAG Glu	TTG Leu	ATT Ile	TCT Ser	GTG Val 710	TCT Ser	GAA Glu	GTC Val	CAC His	CCT Pro	TCT Ser 715	AGA Arg	CTT Leu	CAG Gln	ACC Thr	2161
ACA Thr 720	GAC Asp	AAC Asn	CTG Leu	CTT Leu	CCC Pro 725	ATG Met	TCT Ser	CCA Pro	GAG Glu	GAG Glu 730	TTT Phe	GAT Asp	GAG Glu	ATG Met	TCC Ser 735	2209

1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
 0

CGG ATA GTG GGC CCC GAA TTT GAC AGT ATG ATG AGC ACA GTA  
 Arg Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val  
 740 745

2251

TAAACACGAA TTTCTCTCTG GCGACA

2277

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ser	Gln	Trp	Phe	Glu	Leu	Gln	Gln	Leu	Asp	Ser	Lys	Phe	Leu	Glu	1	5	10	15
Gln	Val	His	Gln	Leu	Tyr	Asp	Asp	Ser	Phe	Pro	Met	Glu	Ile	Arg	Gln	20	25	30	
Tyr	Leu	Ala	Gln	Trp	Leu	Glu	Lys	Gln	Asp	Trp	Glu	His	Ala	Ala	Tyr	35	40	45	
Asp	Val	Ser	Phe	Ala	Thr	Ile	Arg	Phe	His	Asp	Leu	Leu	Ser	Gln	Leu	50	55	60	
Asp	Asp	Gln	Tyr	Ser	Arg	Phe	Ser	Leu	Glu	Asn	Asn	Phe	Leu	Leu	Gln	65	70	75	80
His	Asn	Ile	Arg	Lys	Ser	Lys	Arg	Asn	Leu	Gln	Asp	Asn	Phe	Gln	Glu	85	90	95	
Asp	Pro	Val	Gln	Met	Ser	Met	Ile	Ile	Tyr	Asn	Cys	Leu	Lys	Glu	Glu	100	105	110	
Arg	Lys	Ile	Leu	Glu	Asn	Ala	Gln	Arg	Phe	Asn	Gln	Ala	Gln	Glu	Gly	115	120	125	
Asn	Ile	Gln	Asn	Thr	Val	Met	Leu	Asp	Lys	Gln	Lys	Glu	Leu	Asp	Ser	130	135	140	
Lys	Val	Arg	Asn	Val	Lys	Asp	Gln	Val	Met	Cys	Ile	Glu	Gln	Glu	Ile	145	150	155	160
Lys	Thr	Leu	Glu	Glu	Leu	Gln	Asp	Glu	Tyr	Asp	Phe	Lys	Cys	Lys	Thr	165	170	175	
Ser	Gln	Asn	Arg	Glu	Gly	Glu	Ala	Asn	Gly	Val	Ala	Lys	Ser	Asp	Gln	180	185	190	
Lys	Gln	Glu	Gln	Leu	Leu	Leu	His	Lys	Met	Phe	Leu	Met	Leu	Asp	Asn	195	200	205	
Lys	Arg	Lys	Glu	Ile	Ile	His	Lys	Ile	Arg	Glu	Leu	Leu	Asn	Ser	Ile	210	215	220	
Glu	Leu	Thr	Gln	Asn	Thr	Leu	Ile	Asn	Asp	Glu	Leu	Val	Glu	Trp	Lys	225	230	235	240
Arg	Arg	Gln	Gln	Ser	Ala	Cys	Ile	Gly	Gly	Pro	Pro	Asn	Ala	Cys	Leu	245	250	255	
Asp	Gln	Leu	Gln	Thr	Trp	Phe	Thr	Ile	Val	Ala	Glu	Thr	Leu	Gln	Gln	260	265	270	

Ile	Arg	Gln	Gln	Leu	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Gln	Lys	Phe	Thr
		275					280					285			
Tyr	Glu	Pro	Asp	Pro	Ile	Thr	Lys	Asn	Lys	Gln	Val	Leu	Ser	Asp	Arg
	290					295					300				
Thr	Phe	Leu	Leu	Phe	Gln	Gln	Leu	Ile	Gln	Ser	Ser	Phe	Val	Val	Glu
305					310					315					320
Arg	Gln	Pro	Cys	Met	Pro	Thr	His	Pro	Gln	Arg	Pro	Leu	Val	Leu	Lys
				325					330					335	
Thr	Gly	Val	Gln	Phe	Thr	Val	Lys	Ser	Arg	Leu	Leu	Val	Lys	Leu	Gln
			340					345					350		
Glu	Ser	Asn	Leu	Leu	Thr	Lys	Val	Lys	Cys	His	Phe	Asp	Lys	Asp	Val
		355					360					365			
Asn	Glu	Lys	Asn	Thr	Val	Lys	Gly	Phe	Arg	Lys	Phe	Asn	Ile	Leu	Gly
	370					375					380				
Thr	His	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Thr	Asn	Gly	Ser	Leu
385					390					395					400
Ala	Ala	Glu	Leu	Arg	His	Leu	Gln	Leu	Lys	Glu	Gln	Lys	Asn	Ala	Gly
				405					410					415	
Asn	Arg	Thr	Asn	Glu	Gly	Pro	Leu	Ile	Val	Thr	Glu	Glu	Leu	His	Ser
			420					425					430		
Leu	Ser	Phe	Glu	Thr	Gln	Leu	Cys	Gln	Pro	Gly	Leu	Val	Ile	Asp	Leu
		435					440					445			
Glu	Thr	Thr	Ser	Leu	Pro	Val	Val	Val	Ile	Ser	Asn	Val	Ser	Gln	Leu
	450					455					460				
Pro	Ser	Gly	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	Asn	Met	Leu	Val	Thr	Glu
465					470					475					480
Pro	Arg	Asn	Leu	Ser	Phe	Phe	Leu	Asn	Pro	Pro	Cys	Ala	Trp	Trp	Ser
				485					490					495	
Gln	Leu	Ser	Glu	Val	Leu	Ser	Trp	Gln	Phe	Ser	Ser	Val	Thr	Lys	Arg
			500					505					510		
Gly	Leu	Asn	Ala	Asp	Gln	Leu	Ser	Met	Leu	Gly	Glu	Lys	Leu	Leu	Gly
		515					520					525			
Pro	Asn	Ala	Gly	Pro	Asp	Gly	Leu	Ile	Pro	Trp	Thr	Arg	Phe	Cys	Lys
	530					535					540				
Glu	Asn	Ile	Asn	Asp	Lys	Asn	Phe	Ser	Phe	Trp	Pro	Trp	Ile	Asp	Thr
545					550					555					560
Ile	Leu	Glu	Leu	Ile	Lys	Asn	Asp	Leu	Leu	Cys	Leu	Trp	Asn	Asp	Gly
				565					570					575	
Cys	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	Arg	Glu	Arg	Ala	Leu	Leu	Lys
			580					585					590		
Asp	Gln	Gln	Pro	Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	Ser	Arg
		595					600					605			
Glu	Gly	Ala	Ile	Thr	Phe	Thr	Trp	Val	Glu	Arg	Ser	Gln	Asn	Gly	Gly
	610					615					620				
Glu	Pro	As													



Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala  
645 650 655

Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp  
660 665 670

Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro  
675 680 685

Glu Pro Met Glu Leu Asp Asp Pro Lys Arg Thr Gly Tyr Ile Lys Thr  
690 695 700

Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr  
705 710 715 720

Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Met Ser Arg  
725 730 735

Ile Val Gly Pro Glu Phe Asp Ser Met Met Ser Thr Val  
740 745

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2375 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: splenic/thymic  
(B) CLONE: Murine 13sf1

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 34..2277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCCACTACC TGGACGGAGA GAGAGAGAGC AGC ATG TCT CAG TGG AAT CAA GTC	54
Met Ser Gln Trp Asn Gln Val	
1 5	
CAA CAA TTA GAA ATC AAG TTT TTG GAG CAA GTA GAT CAG TTC TAT GAT	102
Gln Gln Leu Glu Ile Lys Phe Leu Glu Gln Val Asp Gln Phe Tyr Asp	
10 15 20	
GAC AAC TTT CCT ATG GAA ATC CGG CAT CTG CTA GCT CAG TGG ATT GAG	150
Asp Asn Phe Pro Met Glu Ile Arg His Leu Leu Ala Gln Trp Ile Glu	
25 30 35	
ACT CAA GAC TGG GAA GTA GCT TCT AAC AAT GAA ACT ATG GCA ACA ATT	198
Thr Gln Asp Trp Glu Val Ala Ser Asn Asn Glu Thr Met Ala Thr Ile	
40 45 50 55	
CTG CTT CAA AAC TTA CTA ATA CAA TTG GAT GAA CAG TTG GGG CGG GTT	246
Leu Leu Gln Asn Leu Leu Ile Gln Leu Asp Glu Gln Leu Gly Arg Val	
60 65 70	

TCC AAA GAA AAA AAT CTG CTA TTG ATT CAC AAT CTA AAG AGA ATT AGA Ser Lys Glu Lys Asn Leu Leu Leu Ile His Asn Leu Lys Arg Ile Arg	294
75 80 85	
AAA GTT CTT CAG GGC AAG TTT CAT GGA AAT CCA ATG CAT GTA GCT GTG Lys Val Leu Gln Gly Lys Phe His Gly Asn Pro Met His Val Ala Val	342
90 95 100	
GTA ATT TCA AAT TGC TTA AGG GAA GAG AGG AGA ATA TTG GCT GCA GCC Val Ile Ser Asn Cys Leu Arg Glu Glu Arg Arg Ile Leu Ala Ala Ala	390
105 110 115	
AAC ATG CCT ATC CAG GGA CCT CTG GAG AAA TCC TTA CAG AGT TCT TCA Asn Met Pro Ile Gln Gly Pro Leu Glu Lys Ser Leu Gln Ser Ser Ser	438
120 125 130 135	
GTT TCT GAA AGA CAA AGG AAT GTG GAA CAC AAA GTG TCT GCC ATT AAA Val Ser Glu Arg Gln Arg Asn Val Glu His Lys Val Ser Ala Ile Lys	486
140 145 150	
AAC AGT GTG CAG ATG ACA GAA CAA GAT ACC AAA TAC TTA GAA GAC CTG Asn Ser Val Gln Met Thr Glu Gln Asp Thr Lys Tyr Leu Glu Asp Leu	534
155 160 165	
CAA GAT GAG TTT GAC TAC AGG TAT AAA ACA ATT CAG ACA ATG GAT CAG Gln Asp Glu Phe Asp Tyr Arg Tyr Lys Thr Ile Gln Thr Met Asp Gln	582
170 175 180	
GGT GAC AAA AAC AGT ATC CTG GTG AAC CAG GAA GTT TTG ACA CTG CTG Gly Asp Lys Asn Ser Ile Leu Val Asn Gln Glu Val Leu Thr Leu Leu	630
185 190 195	
CAA GAA ATG CTT AAT AGT CTG GAC TTC AAG AGA AAG GAA GCA CTC AGT Gln Glu Met Leu Asn Ser Leu Asp Phe Lys Arg Lys Glu Ala Leu Ser	678
200 205 210 215	
AAG ATG ACG CAG ATA GTG AAC GAG ACA GAC CTG CTC ATG AAC AGC ATG Lys Met Thr Gln Ile Val Asn Glu Thr Asp Leu Leu Met Asn Ser Met	726
220 225 230	
CTT CTA GAA GAG CTG CAG GAC TGG AAA AAG CGG CAC AGG ATT GCC TGC Leu Leu Glu Glu Leu Gln Asp Trp Lys Lys Arg His Arg Ile Ala Cys	774
235 240 245	
ATT GGT GGC CCG CTC CAC AAT GGG CTG GAC CAG CTT CAG AAC TGC TTT Ile Gly Gly Pro Leu His Asn Gly Leu Asp Gln Leu Gln Asn Cys Phe	822
250 255 260	
ACC CTA CTG GCA GAG AGT CTT TTC CAA CTC AGA CAG CAA CTG GAG AAA Thr Leu Leu Ala Glu Ser Leu Phe Gln Leu Arg Gln Gln Leu Glu Lys	870
265 270 275	
CTA CAG GAG CAA TCT ACT AAA ATG ACC TAT GAA GGG GAT CCC ATC CCT Leu Gln Glu Gln Ser Thr Lys Met Thr Tyr Glu Gly Asp Pro Ile Pro	918
280 285 290 295	
GCT CAA AGA GCA CAC CTC CTG GAA AGA GCT ACC TTC CTG ATC TAC AAC Ala Gln Arg Ala His Leu Leu Glu Arg Ala Thr Phe Leu Ile Tyr Asn	966
300 305 310	
CTT TTC AAG AAC TCA TTT GTG GTC GAG CGA CAC GCA TGC ATG CCA ACG Leu Phe Lys Asn Ser Phe Val Val Glu Arg His Ala Cys Met Pro Thr	1014
315 320 325	
CAC CCT CAG AGG CCG ATG GTA CTT AAA ACC CTC ATT CAG TTC ACT GTA His Pro Gln Arg Pro Met Val Leu Lys Thr Leu Ile Gln Phe Thr Val	1062
330 335 340	

AAA Lys	CTG Leu	AGA Arg	TTA Leu	CTA Leu	ATA Ile	AAA Lys	TTG Leu	CCG Pro	GAA Glu	CTA Leu	AAC Asn	TAT Tyr	CAG Gln	GTG Val	AAA Lys	1110
	345					350					355					
GTA Val	AAG Lys	GCG Ala	TCC Ser	ATT Ile	GAC Asp	AAG Lys	AAT Asn	GTT Val	TCA Ser	ACT Thr	CTA Leu	AGC Ser	AAT Asn	AGA Arg	AGA Arg	1158
	360				365					370					375	
TTT Phe	GTG Val	CTT Leu	TGT Cys	GGA Gly	ACT Thr	CAC His	GTC Val	AAA Lys	GCT Ala	ATG Met	TCC Ser	AGT Ser	GAG Glu	GAA Glu	TCT Ser	1206
				380					385					390		
TCC Ser	AAT Asn	GGG Gly	AGC Ser	CTC Leu	TCA Ser	GTG Val	GAG Glu	TTA Leu	GAC Asp	ATT Ile	GCA Ala	ACC Thr	CAA Gln	GGA Gly	GAT Asp	1254
			395					400					405			
GAA Glu	GTG Val	CAG Gln	TAC Tyr	TGG Trp	AGT Ser	AAA Lys	GGA Gly	AAC Asn	GAG Glu	GGC Gly	TGC Cys	CAC His	ATG Met	GTG Val	ACA Thr	1302
		410					415					420				
GAG Glu	GAG Glu	TTG Leu	CAT His	TCC Ser	ATA Ile	ACC Thr	TTT Phe	GAG Glu	ACC Thr	CAG Gln	ATC Ile	TGC Cys	CTC Leu	TAT Tyr	GGC Gly	1350
	425					430					435					
CTC Leu	ACC Thr	ATT Ile	AAC Asn	CTA Leu	GAG Glu	ACC Thr	AGC Ser	TCA Ser	TTA Leu	CCT Pro	GTC Val	GTG Val	ATG Met	ATT Ile	TCT Ser	1398
	440				445					450					455	
AAT Asn	GTC Val	AGC Ser	CAA Gln	CTA Leu	CCT Pro	AAT Asn	GCA Ala	TGG Trp	GCA Ala	TCC Ser	ATC Ile	ATT Ile	TGG Trp	TAC Tyr	AAT Asn	1446
				460				465						470		
GTA Val	TCA Ser	ACT Thr	AAC Asn	GAC Asp	TCC Ser	CAG Gln	AAC Asn	TTG Leu	GTT Val	TTC Phe	TTT Phe	AAT Asn	AAC Asn	CCT Pro	CCA Pro	1494
			475					480					485			
TCT Ser	GTC Val	ACT Thr	TTG Leu	GGC Gly	CAA Gln	CTC Leu	CTG Leu	GAA Glu	GTG Val	ATG Met	AGC Ser	TGG Trp	CAA Gln	TTT Phe	TCA Ser	1542
		490					495					500				
TCC Ser	TAT Tyr	GTC Val	GGT Gly	CGT Arg	GGC Gly	CTT Leu	AAT Asn	TCA Ser	GAG Glu	CAG Gln	CTC Leu	AAC Asn	ATG Met	CTG Leu	GCA Ala	1590
	505					510					515					
GAG Glu	AAG Lys	CTC Leu	ACA Thr	GTT Val	CAG Gln	TCT Ser	AAC Asn	TAC Tyr	AAT Asn	GAT Asp	GGT Gly	CAC His	CTC Leu	ACC Thr	TGG Trp	1638
	520				525					530					535	
GCC Ala	AAG Lys	TTC Phe	TGC Cys	AAG Lys	GAA Glu	CAT His	TTG Leu	CCT Pro	GGC Gly	AAA Lys	ACA Thr	TTT Phe	ACC Thr	TTC Phe	TGG Trp	1686
				540					545					550		
ACT Thr	TGG Trp	CTT Leu	GAA Glu	GCA Ala	ATA Ile	TTG Leu	GAC Asp	CTA Leu	ATT Ile	AAA Lys	AAA Lys	CAT His	ATT Ile	CTT Leu	CCC Pro	1734
			555					560				565				
CTC Leu	TGG Trp	ATT Ile	GAT Asp	GGG Gly	TAC Tyr	ATC Ile	ATG Met	GGA Gly	TTT Phe	GTT Val	AGT Ser	AAA Lys	GAG Glu	AAG Lys	GAA Glu	1782
		570				575						580				
CGG Arg	CTT Leu	CTG Leu	CTC Leu	AAA Lys	GAT Asp	AAA Lys	ATG Met	CCT Pro	GGG Gly	ACA Thr	TTT Phe	TTG Leu	TTA Leu	AGA Arg	TTC Phe	1830
	585					590					595					
AGT Ser	GAG Glu	AGC Ser	CAT His	CTT Leu	GGA Gly	GGG Gly	ATA Ile	ACC Thr	TTC Phe	ACC Thr	TGG Trp	GTG Val	GAC Asp	CAA Gln	TCT Ser	1878
	600				605					610					615	

GAA AAT GGA GAA GTG AGA TTC CAC TCT GTA GAA CCC TAC AAC AAA GGG Glu Asn Gly Glu Val Arg Phe His Ser Val Glu Pro Tyr Asn Lys Gly 620 625 630	1926
AGA CTG TCG GCT CTG GCC TTC GCT GAC ATC CTG CGA GAC TAC AAG GTT Arg Leu Ser Ala Leu Ala Phe Ala Asp Ile Leu Arg Asp Tyr Lys Val 635 640 645	1974
ATC ATG GCT GAA AAC ATC CCT GAA AAC CCT CTG AAG TAC CTC TAC CCT Ile Met Ala Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro 650 655 660	2022
GAC ATT CCC AAA GAC AAA GCC TTT GGC AAA CAC TAC AGC TCC CAG CCG Asp Ile Pro Lys Asp Lys Ala Phe Gly Lys His Tyr Ser Ser Gln Pro 665 670 675	2070
TGC GAA GTC TCA AGA CCA ACC GAA CGG GGA GAC AAG GGT TAC GTC CCC Cys Glu Val Ser Arg Pro Thr Glu Arg Gly Asp Lys Gly Tyr Val Pro 680 685 690 695	2118
TCT GTT TTT ATC CCC ATT TCA ACA ATC CGA AGC GAT TCC ACG GAG CCA Ser Val Phe Ile Pro Ile Ser Thr Ile Arg Ser Asp Ser Thr Glu Pro 700 705 710	2166
CAA TCT CCT TCA GAC CTT CTC CCC ATG TCT CCA AGT GCA TAT GCT GTG Gln Ser Pro Ser Asp Leu Leu Pro Met Ser Pro Ser Ala Tyr Ala Val 715 720 725	2214
CTG AGA GAA AAC CTG AGC CCA ACG ACA ATT GAA ACT GCA ATG AAT TCC Leu Arg Glu Asn Leu Ser Pro Thr Thr Ile Glu Thr Ala Met Asn Ser 730 735 740	2262
CCA TAT TCT GCT GAA TGACGGTGCA AACGGACACT TTAAAGAAGG AAGCAGATGA Pro Tyr Ser Ala Glu 745	2317
AACTGGAGAG TGTTCTTTAC CATAGATCAC AATTTATTTTTC TTCGGCTTTG TAAATACC	2375

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Gln Trp Asn Gln Val Gln Gln Leu Glu Ile Lys Phe Leu Glu 1 5 10 15
Gln Val Asp Gln Phe Tyr Asp Asp Asn Phe Pro Met Glu Ile Arg His 20 25 30
Leu Leu Ala Gln Trp Ile Glu Thr Gln Asp Trp Glu Val Ala Ser Asn 35 40 45
Asn Glu Thr Met Ala Thr Ile Leu Leu Gln Asn Leu Leu Ile Gln Leu 50 55 60
Asp Glu Gln Leu Gly Arg Val Ser Lys Glu Lys Asn Leu Leu Leu Ile 65 70 75 80
His Asn Leu Lys Arg Ile Arg Lys Val Leu Gln Gly Lys Phe His Gly 85 90 95

Asn Pro Met His Val Ala Val Val Ile Ser Asn Cys Leu Arg Glu Glu  
 100 105 110  
 Arg Arg Ile Leu Ala Ala Ala Asn Met Pro Ile Gln Gly Pro Leu Glu  
 115 120 125  
 Lys Ser Leu Gln Ser Ser Ser Val Ser Glu Arg Gln Arg Asn Val Glu  
 130 135 140  
 His Lys Val Ser Ala Ile Lys Asn Ser Val Gln Met Thr Glu Gln Asp  
 145 150 155 160  
 Thr Lys Tyr Leu Glu Asp Leu Gln Asp Glu Phe Asp Tyr Arg Tyr Lys  
 165 170 175  
 Thr Ile Gln Thr Met Asp Gln Gly Asp Lys Asn Ser Ile Leu Val Asn  
 180 185 190  
 Gln Glu Val Leu Thr Leu Leu Gln Glu Met Leu Asn Ser Leu Asp Phe  
 195 200 205  
 Lys Arg Lys Glu Ala Leu Ser Lys Met Thr Gln Ile Val Asn Glu Thr  
 210 215 220  
 Asp Leu Leu Met Asn Ser Met Leu Leu Glu Glu Leu Gln Asp Trp Lys  
 225 230 235 240  
 Lys Arg His Arg Ile Ala Cys Ile Gly Gly Pro Leu His Asn Gly Leu  
 245 250 255  
 Asp Gln Leu Gln Asn Cys Phe Thr Leu Leu Ala Glu Ser Leu Phe Gln  
 260 265 270  
 Leu Arg Gln Gln Leu Glu Lys Leu Gln Glu Gln Ser Thr Lys Met Thr  
 275 280 285  
 Tyr Glu Gly Asp Pro Ile Pro Ala Gln Arg Ala His Leu Leu Glu Arg  
 290 295 300  
 Ala Thr Phe Leu Ile Tyr Asn Leu Phe Lys Asn Ser Phe Val Val Glu  
 305 310 315 320  
 Arg His Ala Cys Met Pro Thr His Pro Gln Arg Pro Met Val Leu Lys  
 325 330 335  
 Thr Leu Ile Gln Phe Thr Val Lys Leu Arg Leu Leu Ile Lys Leu Pro  
 340 345 350  
 Glu Leu Asn Tyr Gln Val Lys Val Lys Ala Ser Ile Asp Lys Asn Val  
 355 360 365  
 Ser Thr Leu Ser Asn Arg Arg Phe Val Leu Cys Gly Thr His Val Lys  
 370 375 380  
 Ala Met Ser Ser Glu Glu Ser Ser Asn Gly Ser Leu Ser Val Glu Leu  
 385 390 395 400  
 Asp Ile Ala Thr Gln Gly Asp Glu Val Gln Tyr Trp Ser Lys Gly Asn  
 405 410 415  
 Glu Gly Cys His Met Val Thr Glu Glu Leu His Ser Ile Thr Phe Glu  
 420 425 430  
 Thr Gln Ile Cys Leu Tyr Gly Leu Thr Ile Asn Leu Glu Thr Ser Ser  
 435 440 445  
 Leu Pro Val Val Met Ile Ser Asn Val Ser Gln Leu Pro Asn Ala Trp  
 450 455 460

Ala	Ser	Ile	Ile	Trp	Tyr	Asn	Val	Ser	Thr	Asn	Asp	Ser	Gln	Asn	Leu	465	470	475	480
Val	Phe	Phe	Asn	Asn	Pro	Pro	Ser	Val	Thr	Leu	Gly	Gln	Leu	Leu	Glu		485	490	495
Val	Met	Ser	Trp	Gln	Phe	Ser	Ser	Tyr	Val	Gly	Arg	Gly	Leu	Asn	Ser	500	505	510	
Glu	Gln	Leu	Asn	Met	Leu	Ala	Glu	Lys	Leu	Thr	Val	Gln	Ser	Asn	Tyr	515	520	525	
Asn	Asp	Gly	His	Leu	Thr	Trp	Ala	Lys	Phe	Cys	Lys	Glu	His	Leu	Pro	530	535	540	
Gly	Lys	Thr	Phe	Thr	Phe	Trp	Thr	Trp	Leu	Glu	Ala	Ile	Leu	Asp	Leu	545	550	555	560
Ile	Lys	Lys	His	Ile	Leu	Pro	Leu	Trp	Ile	Asp	Gly	Tyr	Ile	Met	Gly	565	570	575	
Phe	Val	Ser	Lys	Glu	Lys	Glu	Arg	Leu	Leu	Leu	Lys	Asp	Lys	Met	Pro	580	585	590	
Gly	Thr	Phe	Leu	Leu	Arg	Phe	Ser	Glu	Ser	His	Leu	Gly	Gly	Ile	Thr	595	600	605	
Phe	Thr	Trp	Val	Asp	Gln	Ser	Glu	Asn	Gly	Glu	Val	Arg	Phe	His	Ser	610	615	620	
Val	Glu	Pro	Tyr	Asn	Lys	Gly	Arg	Leu	Ser	Ala	Leu	Ala	Phe	Ala	Asp	625	630	635	640
Ile	Leu	Arg	Asp	Tyr	Lys	Val	Ile	Met	Ala	Glu	Asn	Ile	Pro	Glu	Asn	645	650	655	
Pro	Leu	Lys	Tyr	Leu	Tyr	Pro	Asp	Ile	Pro	Lys	Asp	Lys	Ala	Phe	Gly	660	665	670	
Lys	His	Tyr	Ser	Ser	Gln	Pro	Cys	Glu	Val	Ser	Arg	Pro	Thr	Glu	Arg	675	680	685	
Gly	Asp	Lys	Gly	Tyr	Val	Pro	Ser	Val	Phe	Ile	Pro	Ile	Ser	Thr	Ile	690	695	700	
Arg	Ser	Asp	Ser	Thr	Glu	Pro	Gln	Ser	Pro	Ser	Asp	Leu	Leu	Pro	Met	705	710	715	720
Ser	Pro	Ser	Ala	Tyr	Ala	Val	Leu	Arg	Glu	Asn	Leu	Ser	Pro	Thr	Thr	725	730	735	
Ile	Glu	Thr	Ala	Met	Asn	Ser	Pro	Tyr	Ser	Ala	Glu					740	745		

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2869 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: splenic/thymic

(B) CLONE: Murine 19sf6

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 69..2378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCGCGACCA GCCAGGCCGG CCAGTCGGGC TCAGCCCGGA GACAGTCGAG ACCCCTGACT	60
GCAGCAGG ATG GCT CAG TGG AAC CAG CTG CAG CAG CTG GAC ACA CGC TAC	110
Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr	
1 5 10	
CTG AAG CAG CTG CAC CAG CTG TAC AGC GAC ACG TTC CCC ATG GAG CTG	158
Leu Lys Gln Leu His Gln Leu Tyr Ser Asp Thr Phe Pro Met Glu Leu	
15 20 25 30	
CGG CAG TTC CTG GCA CCT TGG ATT GAG AGT CAA GAC TGG GCA TAT GCA	206
Arg Gln Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala	
35 40 45	
GCC AGC AAA GAG TCA CAT GCC ACG TTG GTG TTT CAT AAT CTC TTG GGT	254
Ala Ser Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly	
50 55 60	
GAA ATT GAC CAG CAA TAT AGC CGA TTC CTG CAA GAG TCC AAT GTC CTC	302
Glu Ile Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu	
65 70 75	
TAT CAG CAC AAC CTT CGA AGA ATC AAG CAG TTT CTG CAG AGC AGG TAT	350
Tyr Gln His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr	
80 85 90	
CTT GAG AAG CCA ATG GAA ATT GCC CGG ATC GTG GCC CGA TGC CTG TGG	398
Leu Glu Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp	
95 100 105 110	
GAA GAG TCT CGC CTC CTC CAG ACG GCA GCC ACG GCA GCC CAG CAA GGG	446
Glu Glu Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly	
115 120 125	
GGC CAG GCC AAC CAC CCA ACA GCC GCC GTA GTG ACA GAG AAG CAG CAG	494
Gly Gln Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln	
130 135 140	
ATG TTG GAG CAG CAT CTT CAG GAT GTC CGG AAG CGA GTG CAG GAT CTA	542
Met Leu Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu	
145 150 155	
GAA CAG AAA ATG AAG GTG GTG GAG AAC CTC CAG GAC GAC TTT GAT TTC	590
Glu Gln Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe	
160 165 170	
AAC TAC AAA ACC CTC AAG AGC CAA GGA GAC ATG CAG GAT CTG AAT GGA	638
Asn Tyr Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly	
175 180 185 190	
AAC AAC CAG TCT GTG ACC AGA CAG AAG ATG CAG CAG CTG GAA CAG ATG	686
Asn Asn Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met	
195 200 205	

CTC	ACA	GCC	CTG	GAC	CAG	ATG	CGG	AGA	AGC	ATT	GTG	AGT	GAG	CTG	GCG	734
Leu	Thr	Ala	Leu	Asp	Gln	Met	Arg	Arg	Ser	Ile	Val	Ser	Glu	Leu	Ala	
			210					215					220			
GGG	CTC	TTG	TCA	GCA	ATG	GAG	TAC	GTG	CAG	AAG	ACA	CTG	ACT	GAT	GAA	782
Gly	Leu	Leu	Ser	Ala	Met	Glu	Tyr	Val	Gln	Lys	Thr	Leu	Thr	Asp	Glu	
		225					230					235				
GAG	CTG	GCT	GAC	TGG	AAG	AGG	CGG	CCA	GAG	ATC	GCG	TGC	ATC	GGA	GGC	830
Glu	Leu	Ala	Asp	Trp	Lys	Arg	Arg	Pro	Glu	Ile	Ala	Cys	Ile	Gly	Gly	
	240					245					250					
CCT	CCC	AAC	ATC	TGC	CTG	GAC	CGT	CTG	GAA	AAC	TGG	ATA	ACT	TCA	TTA	878
Pro	Pro	Asn	Ile	Cys	Leu	Asp	Arg	Leu	Glu	Asn	Trp	Ile	Thr	Ser	Leu	
255					260					265					270	
GCA	GAA	TCT	CAA	CTT	CAG	ACC	CGC	CAA	CAA	ATT	AAG	AAA	CTG	GAG	GAG	926
Ala	Glu	Ser	Gln	Leu	Gln	Thr	Arg	Gln	Gln	Ile	Lys	Lys	Leu	Glu	Glu	
				275					280					285		
CTG	CAG	CAG	AAA	GTG	TCC	TAC	AAG	GGC	GAC	CCT	ATC	GTG	CAG	CAC	CGG	974
Leu	Gln	Gln	Lys	Val	Ser	Tyr	Lys	Gly	Asp	Pro	Ile	Val	Gln	His	Arg	
			290					295					300			
CCC	ATG	CTG	GAG	GAG	AGG	ATC	GTG	GAG	CTG	TTC	AGA	AAC	TTA	ATG	AAG	1022
Pro	Met	Leu	Glu	Glu	Arg	Ile	Val	Glu	Leu	Phe	Arg	Asn	Leu	Met	Lys	
		305					310					315				
AGT	GCC	TTC	GTG	GTG	GAG	CGG	CAG	CCC	TGC	ATG	CCC	ATG	CAC	CCG	GAC	1070
Ser	Ala	Phe	Val	Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Met	His	Pro	Asp	
	320					325					330					
CGG	CCC	TTA	GTC	ATC	AAG	ACT	GGT	GTC	CAG	TTT	ACC	ACG	AAA	GTC	AGG	1118
Arg	Pro	Leu	Val	Ile	Lys	Thr	Gly	Val	Gln	Phe	Thr	Thr	Lys	Val	Arg	
335					340					345					350	
TTG	CTG	GTC	AAA	TTT	CCT	GAG	TTG	AAT	TAT	CAG	CTT	AAA	ATT	AAA	GTG	1166
Leu	Leu	Val	Lys	Phe	Pro	Glu	Leu	Asn	Tyr	Gln	Leu	Lys	Ile	Lys	Val	
				355					360					365		
TGC	ATT	GAT	AAA	GAC	TCT	GGG	GAT	GTT	GCT	GCC	CTC	AGA	GGG	TCT	CGG	1214
Cys	Ile	Asp	Lys	Asp	Ser	Gly	Asp	Val	Ala	Ala	Leu	Arg	Gly	Ser	Arg	
			370					375					380			
AAA	TTT	AAC	ATT	CTG	GGC	ACG	AAC	ACA	AAA	GTG	ATG	AAC	ATG	GAG	GAG	1262
Lys	Phe	Asn	Ile	Leu	Gly	Thr	Asn	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	
		385					390					395				
TCT	AAC	AAC	GGC	AGC	CTG	TCT	GCA	GAG	TTC	AAG	CAC	CTG	ACC	CTT	AGG	1310
Ser	Asn	Asn	Gly	Ser	Leu	Ser	Ala	Glu	Phe	Lys	His	Leu	Thr	Leu	Arg	
	400					405					410					
GAG	CAG	AGA	TGT	GGG	AAT	GGA	GGC	CGT	GCC	AAT	TGT	GAT	GCC	TCC	TTG	1358
Glu	Gln	Arg	Cys	Gly	Asn	Gly	Gly	Arg	Ala	Asn	Cys	Asp	Ala	Ser	Leu	
415					420					425					430	
ATC	GTG	ACT	GAG	GAG	CTG	CAC	CTG	ATC	ACC	TTC	GAG	ACT	GAG	GTG	TAC	1406
Ile	Val	Thr	Glu	Glu	Leu	His	Leu	Ile	Thr	Phe	Glu	Thr	Glu	Val	Tyr	
				435					440					445		
CAC	CAA	GGC	CTC	AAG	ATT	GAC	CTA	GAG	ACC	CAC	TCC	TTG	CCA	GTT	GTG	1454
His	Gln	Gly	Leu	Lys	Ile	Asp	Leu	Glu	Thr	His	Ser	Leu	Pro	Val	Val	
			450					455					460			
GTG	ATC	TCC	AAC	ATC	TGT	CAG	ATG	CCA	AAT	GCT	TGG	GCA	TCA	ATC	CTG	1502
Val	Ile	Ser	Asn	Ile	Cys	Gln	Met	Pro	Asn	Ala	Trp	Ala	Ser	Ile	Leu	
		465					470					475				



TGG	TAT	AAC	ATG	CTG	ACC	AAT	AAC	CCC	AAG	AAC	GTG	AAC	TTC	TTC	ACT	1550
Trp	Tyr	Asn	Met	Leu	Thr	Asn	Asn	Pro	Lys	Asn	Val	Asn	Phe	Phe	Thr	
480						485					490					
AAG	CCG	CCA	ATT	GGA	ACC	TGG	GAC	CAA	GTG	GCC	GAG	GTG	CTC	AGC	TGG	1598
Lys	Pro	Pro	Ile	Gly	Thr	Trp	Asp	Gln	Val	Ala	Glu	Val	Leu	Ser	Trp	
495					500					505					510	
CAG	TTC	TCG	TCC	ACC	ACC	AAG	CGA	GGG	CTG	AGC	ATC	GAG	CAG	CTG	ACA	1646
Gln	Phe	Ser	Ser	Thr	Thr	Lys	Arg	Gly	Leu	Ser	Ile	Glu	Gln	Leu	Thr	
				515					520					525		
ACG	CTG	GCT	GAG	AAG	CTC	CTA	GGG	CCT	GGT	GTG	AAC	TAC	TCA	GGG	TGT	1694
Thr	Leu	Ala	Glu	Lys	Leu	Leu	Gly	Pro	Gly	Val	Asn	Tyr	Ser	Gly	Cys	
			530					535					540			
CAG	ATC	ACA	TGG	GCT	AAA	TTC	TGC	AAA	GAA	AAC	ATG	GCT	GGC	AAG	GGC	1742
Gln	Ile	Thr	Trp	Ala	Lys	Phe	Cys	Lys	Glu	Asn	Met	Ala	Gly	Lys	Gly	
		545					550					555				
TTC	TCC	TTC	TGG	GTC	TGG	CTA	GAC	AAT	ATC	ATC	GAC	CTT	GTG	AAA	AAG	1790
Phe	Ser	Phe	Trp	Val	Trp	Leu	Asp	Asn	Ile	Ile	Asp	Leu	Val	Lys	Lys	
	560					565					570					
TAT	ATC	TTG	GCC	CTT	TGG	AAT	GAA	GGG	TAC	ATC	ATG	GGT	TTC	ATC	AGC	1838
Tyr	Ile	Leu	Ala	Leu	Trp	Asn	Glu	Gly	Tyr	Ile	Met	Gly	Phe	Ile	Ser	
575					580					585					590	
AAG	GAG	CGG	GAG	CGG	GCC	ATC	CTA	AGC	ACA	AAG	CCC	CCG	GGC	ACC	TTC	1886
Lys	Glu	Arg	Glu	Arg	Ala	Ile	Leu	Ser	Thr	Lys	Pro	Pro	Gly	Thr	Phe	
				595					600					605		
CTA	CTG	CGC	TTC	AGC	GAG	AGC	AGC	AAA	GAA	GGA	GGG	GTC	ACT	TTC	ACT	1934
Leu	Leu	Arg	Phe	Ser	Glu	Ser	Ser	Lys	Glu	Gly	Gly	Val	Thr	Phe	Thr	
			610					615					620			
TGG	GTG	GAA	AAG	GAC	ATC	AGT	GGC	AAG	ACC	CAG	ATC	CAG	TCT	GTA	GAG	1982
Trp	Val	Glu	Lys	Asp	Ile	Ser	Gly	Lys	Thr	Gln	Ile	Gln	Ser	Val	Glu	
		625					630					635				
CCA	TAC	ACC	AAG	CAG	CAG	CTG	AAC	AAC	ATG	TCA	TTT	GCT	GAA	ATC	ATC	2030
Pro	Tyr	Thr	Lys	Gln	Gln	Leu	Asn	Asn	Met	Ser	Phe	Ala	Glu	Ile	Ile	
	640					645					650					
ATG	GGC	TAT	AAG	ATC	ATG	GAT	GCG	ACC	AAC	ATC	CTG	GTG	TCT	CCA	CTT	2078
Met	Gly	Tyr	Lys	Ile	Met	Asp	Ala	Thr	Asn	Ile	Leu	Val	Ser	Pro	Leu	
655					660					665					670	
GTC	TAC	CTC	TAC	CCC	GAC	ATT	CCC	AAG	GAG	GAG	GCA	TTT	GGA	AAG	TAC	2126
Val	Tyr	Leu	Tyr	Pro	Asp	Ile	Pro	Lys	Glu	Glu	Ala	Phe	Gly	Lys	Tyr	
				675					680					685		
TGT	AGG	CCC	GAG	AGC	CAG	GAG	CAC	CCC	GAA	GCC	GAC	CCA	GGT	AGT	GCT	2174
Cys	Arg	Pro	Glu	Ser	Gln	Glu	His	Pro	Glu	Ala	Asp	Pro	Gly	Ser	Ala	
			690					695					700			
GCC	CCG	TAC	CTG	AAG	ACC	AAG	TTC	ATC	TGT	GTG	ACA	CCA	ACG	ACC	TGC	2222
Ala	Pro	Tyr	Leu	Lys	Thr	Lys	Phe	Ile	Cys	Val	Thr	Pro	Thr	Thr	Cys	
		705					710					715				
AGC	AAT	ACC	ATT	GAC	CTG	CCG	ATG	TCC	CCC	CGC	ACT	TTA	GAT	TCA	TTG	2270
Ser	Asn	Thr	Ile	Asp	Leu	Pro	Met	Ser	Pro	Arg	Thr	Leu	Asp	Ser	Leu	
	720					725					730					
ATG	CAG	TTT	GGA	AAT	AAC	GGT	GAA	GGT	GCT	GAG	CCC	TCA	GCA	GGA	GGG	2318
Met	Gln	Phe	Gly	Asn	Asn	Gly	Glu	Gly	Ala	Glu	Pro	Ser	Ala	Gly	Gly	
735					740					745					750	

CAG TTT GAG TCG CTC ACG TTT GAC ATG GAT CTG ACC TCG GAG TGT GCT	2366
Gln Phe Glu Ser Leu Thr Phe Asp Met Asp Leu Thr Ser Glu Cys Ala	
755 760 765	
ACC TCC CCC ATG TGAGGAGCTG AAACCAGAAG CTGCAGAGAC GTGACTTGAG	2418
Thr Ser Pro Met	
770	
ACACCTGCCC CGTGCTCCAC CCCTAAGCAG CCGAACCCCA TATCGTCTGA AACTCCTAAC	2478
TTTGTGGTTC CAGATTTTTT TTTTAAATTT CCTACTTCTG CTATCTTTGG GCAATCTGGG	2538
CACTTTTAA AAGAGAGAAA TGAGTGAGTG TGGGTGATAA ACTGTTATGT AAAGAGGAGA	2598
GACCTCTGAG TCTGGGGATG GGGCTGAGAG CAGAAGGGAG GCAAAGGGGA ACACCTCCTG	2658
TCCTGCCCCG CTGCCCTCCT TTTTCAGCAG CTCGGGGGTT GGTGTGTTAGA CAAGTGCCTC	2718
CTGGTGCCCA TGGCTACCTG TTGCCCCACT CTGTGAGCTG ATACCCCAT CTGGGAACCT	2778
CTGGCTCTGC ACTTTCAACC TTGCTAATAT CCACATAGAA GCTAGGACTA AGCCCAGGAG	2838
GTTCCTCTTT AAATTAAAAA AAAAAAAAAA A	2869

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 770 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ala	Gln	Trp	Asn	Gln	Leu	Gln	Gln	Leu	Asp	Thr	Arg	Tyr	Leu	Lys
1				5					10					15	
Gln	Leu	His	Gln	Leu	Tyr	Ser	Asp	Thr	Phe	Pro	Met	Glu	Leu	Arg	Gln
		20						25					30		
Phe	Leu	Ala	Pro	Trp	Ile	Glu	Ser	Gln	Asp	Trp	Ala	Tyr	Ala	Ala	Ser
		35						40					45		
Lys	Glu	Ser	His	Ala	Thr	Leu	Val	Phe	His	Asn	Leu	Leu	Gly	Glu	Ile
	50					55					60				
Asp	Gln	Gln	Tyr	Ser	Arg	Phe	Leu	Gln	Glu	Ser	Asn	Val	Leu	Tyr	Gln
65					70					75					80
His	Asn	Leu	Arg	Arg	Ile	Lys	Gln	Phe	Leu	Gln	Ser	Arg	Tyr	Leu	Glu
			85					90						95	
Lys	Pro	Met	Glu	Ile	Ala	Arg	Ile	Val	Ala	Arg	Cys	Leu	Trp	Glu	Glu
		100						105					110		
Ser	Arg	Leu	Leu	Gln	Thr	Ala	Ala	Thr	Ala	Ala	Gln	Gln	Gly	Gly	Gln
		115				120						125			
Ala	Asn	His	Pro	Thr	Ala	Ala	Val	Val	Thr	Glu	Lys	Gln	Gln	Met	Leu
		130				135					140				
Glu	Gln	His	Leu	Gln	Asp	Val	Arg	Lys	Arg	Val	Gln	Asp	Leu	Glu	Gln
145					150					155					160
Lys	Met	Lys	Val	Val	Glu	Asn	Leu	Gln	Asp	Asp	Phe	Asp	Phe	Asn	Tyr
				165					170					175	

Lys	Thr	Leu	Lys 180	Ser	Gln	Gly	Asp	Met 185	Gln	Asp	Leu	Asn	Gly 190	Asn	Asn	
Gln	Ser	Val 195	Thr	Arg	Gln	Lys	Met 200	Gln	Gln	Leu	Glu	Gln	Met	Leu	Thr	
Ala	Leu	Asp	Gln	Met	Arg	Arg	Ser	Ile	Val	Ser	Glu	Leu	Ala	Gly	Leu	
Leu	Ser	Ala	Met	Glu	Tyr 230	Val	Gln	Lys	Thr	Leu	Thr	Asp	Glu	Glu	Leu	
Ala	Asp	Trp	Lys	Arg 245	Arg	Pro	Glu	Ile	Ala 250	Cys	Ile	Gly	Gly	Pro	Pro	
Asn	Ile	Cys	Leu 260	Asp	Arg	Leu	Glu	Asn	Trp	Ile	Thr	Ser	Leu	Ala	Glu	
Ser	Gln	Leu	Gln	Thr	Arg	Gln	Gln	Ile	Lys	Lys	Leu	Glu	Glu	Leu	Gln	
Gln	Lys 290	Val	Ser	Tyr	Lys	Gly 295	Asp	Pro	Ile	Val	Gln	His	Arg	Pro	Met	
Leu	Glu	Glu	Arg	Ile	Val	Glu	Leu	Phe	Arg	Asn	Leu	Met	Lys	Ser	Ala	
Phe	Val	Val	Glu	Arg	Gln	Pro	Cys	Met	Pro	Met	His	Pro	Asp	Arg	Pro	
Leu	Val	Ile	Lys 340	Thr	Gly	Val	Gln	Phe	Thr	Thr	Lys	Val	Arg	Leu	Leu	
Val	Lys	Phe 355	Pro	Glu	Leu	Asn	Tyr 360	Gln	Leu	Lys	Ile	Lys	Val	Cys	Ile	
Asp	Lys 370	Asp	Ser	Gly	Asp	Val	Ala	Ala	Leu	Arg	Gly	Ser	Arg	Lys	Phe	
Asn	Ile	Leu	Gly	Thr	Asn	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Asn	
Asn	Gly	Ser	Leu	Ser	Ala	Glu	Phe	Lys	His	Leu	Thr	Leu	Arg	Glu	Gln	
Arg	Cys	Gly	Asn	Gly	Gly	Arg	Ala	Asn	Cys	Asp	Ala	Ser	Leu	Ile	Val	
Thr	Glu	Glu	Leu	His	Leu	Ile	Thr	Phe	Glu	Thr	Glu	Val	Tyr	His	Gln	
Gly	Leu	Lys	Ile	Asp	Leu	Glu	Thr	His	Ser	Leu	Pro	Val	Val	Val	Ile	
Ser	Asn	Ile	Cys	Gln	Met	Pro	Asn	Ala	Trp	Ala	Ser	Ile	Leu	Trp	Tyr	
Asn	Met	Leu	Thr	Asn	Asn	Pro	Lys	Asn	Val	Asn	Phe	Phe	Thr	Lys	Pro	
Pro	Ile	Gly	Thr	Trp	Asp	Gln	Val	Ala	Glu	Val	Leu	Ser	Trp	Gln	Phe	
Ser	Ser	Thr	Thr	Lys	Arg	Gly	Leu	Ser	Ile	Glu	Gln	Leu	Thr	Thr	Leu	
Ala	Glu	Lys	Leu	Leu	Gly	Pro	Gly	Val	Asn	Tyr	Ser	Gly	Cys	Gln	Ile	

Thr	Trp	Ala	Lys	Phe	Cys	Lys	Glu	Asn	Met	Ala	Gly	Lys	Gly	Phe	Ser	545	550	555	560
Phe	Trp	Val	Trp	Leu	Asp	Asn	Ile	Ile	Asp	Leu	Val	Lys	Lys	Tyr	Ile	565	570	575	
Leu	Ala	Leu	Trp	Asn	Glu	Gly	Tyr	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu	580	585	590	
Arg	Glu	Arg	Ala	Ile	Leu	Ser	Thr	Lys	Pro	Pro	Gly	Thr	Phe	Leu	Leu	595	600	605	
Arg	Phe	Ser	Glu	Ser	Ser	Lys	Glu	Gly	Gly	Val	Thr	Phe	Thr	Trp	Val	610	615	620	
Glu	Lys	Asp	Ile	Ser	Gly	Lys	Thr	Gln	Ile	Gln	Ser	Val	Glu	Pro	Tyr	625	630	635	640
Thr	Lys	Gln	Gln	Leu	Asn	Asn	Met	Ser	Phe	Ala	Glu	Ile	Ile	Met	Gly	645	650	655	
Tyr	Lys	Ile	Met	Asp	Ala	Thr	Asn	Ile	Leu	Val	Ser	Pro	Leu	Val	Tyr	660	665	670	
Leu	Tyr	Pro	Asp	Ile	Pro	Lys	Glu	Glu	Ala	Phe	Gly	Lys	Tyr	Cys	Arg	675	680	685	
Pro	Glu	Ser	Gln	Glu	His	Pro	Glu	Ala	Asp	Pro	Gly	Ser	Ala	Ala	Pro	690	695	700	
Tyr	Leu	Lys	Thr	Lys	Phe	Ile	Cys	Val	Thr	Pro	Thr	Thr	Cys	Ser	Asn	705	710	715	720
Thr	Ile	Asp	Leu	Pro	Met	Ser	Pro	Arg	Thr	Leu	Asp	Ser	Leu	Met	Gln	725	730	735	
Phe	Gly	Asn	Asn	Gly	Glu	Gly	Ala	Glu	Pro	Ser	Ala	Gly	Gly	Gln	Phe	740	745	750	
Glu	Ser	Leu	Thr	Phe	Asp	Met	Asp	Leu	Thr	Ser	Glu	Cys	Ala	Thr	Ser	755	760	765	
Pro	Met															770			

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAAYACNGARC CNATGGARAT YATT

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAYGTTNGAYC ARYTNAAYAT G

21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

RTCDATRTTN GRGTANAR

18

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTAYAANTYR AYCAGNGYAA

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCGAGATG TATTTCCCAG AAAAG

25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu	Asp	Gly	Pro	Lys	Gly	Thr	Gly	Tyr	Ile	Lys	Thr	Glu	Leu	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly	Tyr	Ile	Lys	Thr	Glu
1				5	

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys	Val	Asn	Leu	Gln	Glu	Arg	Arg	Lys	Tyr	Leu	Lys	His	Arg
1				5					10				

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu	Pro	Gln	Tyr	Glu	Glu	Ile	Pro	Ile	Tyr	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: Src

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Waksman, et al.

(C) JOURNAL: Nature  
(D) VOLUME: 358  
(F) PAGES: 646-653  
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg  
1 5 10 15  
Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu  
20 25 30  
Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Phe  
35 40 45  
Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu  
50 55 60  
Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu  
65 70 75 80  
Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His  
85 90 95  
Arg Leu Thr Asn Val Cys Pro Thr Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Abl

(x) PUBLICATION INFORMATION:  
(A) AUTHORS: Overduin, et al.  
(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
(D) VOLUME: 89  
(F) PAGES: 11673-11677  
(G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Asn Ala Ala Glu  
1 5 10 15  
Tyr Leu Leu Ser Ser Gly Ile Asn Gly Ser Phe Leu Val Arg Glu Ser  
20 25 30  
Asp Arg Arg Pro Gly Gln Arg Ser Ile Ser Leu Arg Tyr Glu Glu Gly  
35 40 45  
Arg Val Tyr His Tyr Arg Ile Asn Thr Ala Ser Asp Gly Lys Leu Tyr  
50 55 60



Val Ser Ser Glu Ser Arg Phe Asn Thr Leu Ala Glu Leu Val His His  
65 70 75 80  
His Ser Thr Val Ala Asp Gly Leu Ile Thr Thr Leu His Tyr Pro Ala  
85 90 95  
Pro Lys Arg

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Lck

- (x) PUBLICATION INFORMATION:  
(A) AUTHORS: Eck, et al.  
(C) JOURNAL: Nature  
(D) VOLUME: 362  
(F) PAGES: 87-91  
(G) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Phe Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu  
1 5 10 15  
Ala Pro Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser  
20 25 30  
Thr Ala Gly Ser Phe Ser Leu Ser Val Arg Asp Asp Phe Asp Gln Asn  
35 40 45  
Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly  
50 55 60  
Gly Phe Tyr Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Asp Leu  
65 70 75 80  
Val Arg His Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser  
85 90 95  
Arg Pro Cys Gln Thr Gln  
100

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu Tyr Pro